



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 114184

TO: Minh-Tam Davis
Location: rem/3a24/3c18
Art Unit: 1642
Tuesday, February 24, 2004

Case Serial Number: 10/032159

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Davis,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:41 ; Search time 7900 Seconds

(without alignments)
11268.272 Million cell updates/sec

Title: US-10-032-159a-19

Perfect score: 2176
Sequence: 1 atccaccaggaagtgacacag.....aaacacagcgggtgacccgc 2176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank1: *
1: gb_da: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
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33: em_hcg_mus: *
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40: em_hcg_mus: *
41: em_hcg_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2176	100.0	2176	6	BD160313
2	2176	100.0	2176	9	AK024001
3	1757	80.7	2132	9	AF311287
4	1746	80.2	2098	6	AX154565
5	1448.4	65.6	1608	6	AX154567
6	1423.8	65.4	1836	6	BC008877
7	1060.2	48.7	1879	6	AX154562
8	1060.2	48.7	1879	10	AF311288
9	1045	48.0	1608	6	AX154564
10	725.4	33.3	765	6	BD150612
11	398	18.3	413	6	BD155532
12	389.8	17.9	188462	9	AL592301
13	374.8	17.2	2031	5	AB066061
14	373.8	17.2	4085	10	AY135367
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20	365.8	16.8	2595	9	BC035805
21	323	14.8	179270	10	AC121918
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24	264	12.1	3908	9	AY032928
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34	149	6.8	105327	5	AC140940
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36	146.4	6.7	160539	2	AC109193
37	144.6	6.6	293592	2	AC094571
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42	132.8	6.1	9551	6	AR076233
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45	132.8	6.1	272545	2	AC090533

ALIGNMENTS

RESULT 1
BD160313 2176 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD160313
VERSION BD160313.1 GI:27866071
KEYWORDS UP 2002191363-A/15156.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2176)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,T.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE
Primer for synthesizing full-length cDNA and use thereof

Db	Accession	Definition	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
Dn	1741	AGCAGCGGGAGGCCGCCCGAGAGAGACGGCGCGCCTCAAAAGAGATTGTGAACTAC									
Qy	1801	CGCAGAGAGCGCGCGCCTCAGAGAGATGCAGAAAGATGCGCGCAGGGGGAGAGAGACCGG									
Dn	1801	CGCAGAGAGCGCGCGCCTCAGAGAGATGCAGAAAGATGCGCGCAGGGGGAGAGAGACCGG									
Qy	1861	GAGAAACACACAGGGGAGAGGACACACACCGACACTGAGGGCTCTCTGACCGCAGACACTTCC									
Dn	1861	GAGAAACACACAGGGGAGAGGACACACACCGACACTGAGGGCTCTCTGACCGCAGACACTTCC									
Qy	1921	CCGAGCGCTGCTGACTTGGCTCTGGAACGAGAGATCTGCTGCTCCCTGAAAGGCCCGACGCCG									
Dn	1921	CCGAGCGCTGCTGACTTGGCTCTGGAACGAGAGATCTGCTGCTCCCTGAAAGGCCCGACGCCG									
Qy	1981	ACTGCGCGGGACATGCGGGCGCGTTGTTGAGCGGACCTCAATTTTGGGAGAGCCATCGGGTG									
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Dn	2041	CTCACACACCCCATGACACACCCCATCTGTGTAACTTCAGATCTGTTCTGTTACCATG									
Qy	2101	TAACACACATATCATATCATATCATATGTTAGTATTTAGAAAACACAGCTCGCTAATAAAC									
Dn	2101	TAACACACATATCATATCATATCATATGTTAGTATTTAGAAAACACAGCTCGCTAATAAAC									
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Dn	2161	AGCAGCGGTGACCCGC	2176								
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DEFINITION		AK024001									
ACCESSION		AK024001									
VERSION		AK024001.1	GI:10435237								
KEYWORDS			oligo capping; fis (full insert sequence).								
SOURCE			Homo sapiens (human)								
ORGANISM			Homo sapiens								
REFERENCE			Bukariyoti, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
AUTHORS			1								
TITLE			Isogai, T., Oca, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shizatori, A., Sudo, H., Magatsuma, M., Hosoi, T., Kaki, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Kurakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, O., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuko, Y., Nimomura, K. and Iwayanagi, T.								
JOURNAL			NEBO human cDNA sequencing project								
COMMENT			Unpublished								
AUTHORS			2 (bases 1 to 2176)								
TITLE			Isogai, T. and Otsuki, T.								
JOURNAL			Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)								
COMMENT			NEBO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.								
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source			1..2176								
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			/cName="Y79A11000827"								
			/cell_line="Y79"								

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BASE COUNT	464 a	657 c	734 g	321 t
ORIGIN				
Query Match	100.0%;	Score 2176;	DB 9;	Length 2176;
Best Local Similarity	100.0%;	Pred. No. 3.5e-311;		
Matches 2176; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0
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Ox	61 TTTCCCAAGAGGCTCCGGCGGCCAAGGCTCTGAGTGTGTCTGATGCAGTGTCCTCGA	120		
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Ox	301 CCAACTCGTGCATTCGCAAAACGAAAGTGGTGTGCTCTGGACATCTCTGCACGACACG	360		
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Ox	361 GCCAACAGGGCTACGAGGCTTCCCTCGAGAGCGTAGAGCTGTACTACCGAGCTGNACA	420		
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QY 781 AGCTAAGACACAGCTTCATGAAAGCCGAGAGCACTGCAAGGTGAGGCGAAGCAACAGC 840
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 DB 841 TGAAGCTCAGGCAAGCCATGAGAGAGGCGCCAGCAGAGAGTCTGTGGAGAGCTGACAGC 900
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 QY 961 AGGTGAG 1020
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 QY 1021 GGGAGCAGCAG 1080
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 QY 1801 CGCAG 1860
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QY 1861 GAGAAACACACAGGAG 1920
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 QY 1921 CCGAG 1980
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 QY 1981 ACTGCGGAG 2040
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 DB 2101 TAAACACACATACAG 2160
 QY 2161 AGCAGGAG 2176
 DB 2161 AGCAGGAG 2176

RESULT 3
 AF311287 2132 bp mRNA linear PRI 10-Jan-2001
 LOCUS Homo sapiens caspase recruitment domain protein 9 mRNA, complete
 DEFINITION
 cde.
 ACCESSION AF311287
 VERSION AF311287.1 GI:11066983
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS 1 (bases 1 to 2132)
 Bertin,J., Guo,X., Wang,L., Srinivasula,S.M., Jacobson,M.D.,
 Poyet,J.-L., Merriam,S., Du,M.Q., Dyer,M.J.S., Robison,K.E.,
 D'Este,F., P. S., and Alnemri,E. S.
 CARD9 is a novel caspase recruitment domain-containing protein that
 interacts with Bcl10/CIAP and activates NF-kappa B
 J. Biol. Chem. 275 (52), 41082-41086 (2000)
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
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QY	2054	TGCAAGCCACTTGTGTGACTGAGATCTGTTCTGTTTACCATTGTAACAGCAATATAC	2113
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Db	2078	CGC 2080	
RESULT 4			
AX154565		2098 bp	DNA linear PAT 22-JUN-2001
LOCUS	AX154565		
DEFINITION	Sequence 4 from Patent WO0140468.		
ACCESSION	AX154565		
VERSION	AX154565.1	GI:14536158	
KEYWORDS			
ORGANISM	Homo sapiens (human)		
SOURCE	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Bertin, J.		
TITLE	Molecules of the card-related protein family and uses thereof		
JOURNAL	Patent: WO 0140468-A 4 07-JUN-2001;		
	Millennium Pharmaceuticals, Inc. (US)		
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ORIGIN			
Query Match	80.2%;	Score 1746;	DB 6; Length 2098;
Best Local Similarity	89.9%;	Pred. No. 86-248;	
Matches 1999;	Conservative	0; Mismatches	5; Indels 220; Gaps 3;
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OY	265	TGAACCTGTATGTAGAGACAGAGTGTCTGAGCGACCCCAACTGTGTATCTCGCAAAAGCA	324
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DEFINITION Sequence 6 from Patent WO0140468.
ACCESSION AX154567
VERSION AX154567.1 GI:14536160
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
1 Bertin, J.
AUTHORS Molecules of the card-related protein family and uses thereof
TITLE Patent: WO 0140468-A 6 07-JUN-2001;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
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ACCESSION BC008877
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1836)
 Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Datchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Ueda, T.B., Yoshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, V.S., Krzywicki, M.I., Skalski, U., Smalins, D.E.,
 Schemm, A., Schein, J.E., Jones, S.J., and Morris, M.A. Genom-
 ics and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 2 (bases 1 to 1836)
 Strauberg, R.
 Direct Submission
 Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIN-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT: MGC help desk
 COMMENT Email: cgabs-remail.nih.gov

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 Location/Qualifiers

DEFINITION Sequence 1 from Patent WO0140468.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
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 AUTHORS
 TITLE Molecules of the card-related protein family and uses thereof
 JOURNAL Patent: WO 0140468-A 1 07-JUN-2001;
 Millennium Pharmaceuticals, Inc. (US)
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VERSION AF311288.1 GI:11066965
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          1 (bases 1 to 1879)
          Bertin,J., Guo,Y., Wang,L., Srinivasula,S.M., Jacobson,M.D.,
          Poyet,J.-L., Merriem,S., Du,M.Q., Dyer,M.J.S., Robison,K.E.,
          DiStefano,P.S. and Alnemri,E.S.
          CARD9 is a novel caspase recruitment domain-containing protein that
          interacts with Bcl10/CLAP and activates NF-kappa B
          J Biol. Chem. 275 (52), 41082-41086 (2000)

JOURNAL 20576268
MEDLINE 11053425
PUBMED 2 (bases 1 to 1879)
REFERENCE Bertin,J.
          Direct Submission
          Submitted (05-OCT-2000) Neurobiology, Millennium Pharmaceuticals,
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Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;
QY      76  GCGGCCACAGGCTCTCGTGTGTGTCTGCAAGTGTGTCTCTGGAAGACCTTGACCTGC 135
Db      46  GTGCCATATAGCCACAGCGACATCCAGCTGAGAGGTGTCTCCACAGACCTTGA---GC 101
QY      136  CTGCTAGAGCCATGTCGAGACTACGAGAACATGACGAGTGTCTGAAACGTCCTGAGGCT 195
Db      102  CTACAGAGACATGTCAACTATGAAATGACAGAGATGTCTGAGTGTCTCTTGAGAGCT 161
QY      196  TCCGGGTACAGCTCACTGTGTCATCGACCCCTCAGCATACACCTTACCTGCGGAGT 255
Db      162  TCCGGGTAGACTAATCTCTGATTCACCCCTCAGCATACACCTTATCTGCGGAGT 221
QY      256  GCAGAGTCTTGAACCTGATGATGAGAGAGAGTGTCTGACGACCCCACTGTGATCC 315
Db      222  GCAAGTCTTGAACCCCGATGATGAGAGAGAGTGTCTGATGACCCCACTGTGATCC 281
QY      316  GCAAACGAAAGTGGGTGTCTCTGACATCTCTGACGAGACCGGCAAGGGCTACG 375
Db      282  GCAGACGAAAGTGGGTGTGTCTCTGACATCTCTGACGAGACCGGCAAGGGCTACG 341
QY      376  TGGCCTTCTGAGAGCCCTGAGAGCTCTACCCGCACTGTATACAGAAAGTCAACAGCA 435
Db      342  TGGCCTTCTTGAAGGTCTGAGACCTTACCTACCTCACTTATACAGAAAGTCACTGCA 401
QY      436  AGAGACCGGCGCGCTCTCTTCATGATCATACGACCTCGCGGAGTCAAGGCTGATCTC 495
Db      402  AGAGACCGGCGGCTCTCTTCATGATCATACGACCTCAAGGAGTCTGAGGCTGAGGC 461
QY      496  AGCTGCTGATGACTGAGGTCTGAAAGCTGCAAGAAAGTGCAGACCTGACCGGCTGC 555
Db      462  AGCTGCTGATGACAGAGGTCTGAAAGCTGCAAGAAAGTGCAGACCTGACCGGCTTC 521
QY      556  TAGCTCCAAAGATGATCTTCAACAGAGAGTGTGCGGTGAAGAGACGCTGTGCGCAGC 615
Db      522  TAGCTCCAAAGATGATCTTCAACAGAGAGTGTGCGGTGAAGAGACGCTGTGCGCAGC 581
QY      616  ACCAGAGAGCTGTGAGAGGCTCAAGAGAGAGTGTGAGGCGCGGCGAGGCTCAAGC 675
Db      582  ACCAGAGAGGAGTGTGAGGCGCTCAAGAGAGAGTGTGAGGCTGAGGCGGAGGCTGAGC 641
QY      676  GCTGCAAGAGAGAGACTTACGACCTGTGCATGCGCTGCGGCAACAGAGTGAAGAAAG 735
Db      642  GCTGCAAGAGATGAGACTTACGACCTGTGCATGCGCTGCGGCAACAGAGTGAAGAAAG 701
QY      736  GCGCGCGCTCATGCGAAACCGTGAACCTGACGTGAGATGACCAAGCTCAAGCAACGCC 795
Db      702  GAGCAGCACTCATGCGAAACCGTGAACCTGACGTGAGATGACCAAGCTCAAGCAACGCC 761
QY      796  TCATGAGGCGCAGAGACGACCTGCAAGGTGAGAGCGCAAGCACGCTGAAAGCTCAGCAGC 855
Db      762  TCATGAGGCGCAGAGATGACTGCAAGGTGAGAGCGCAAGCACGCTGAAAGCTCAGCAGC 821
QY      856  CCATGAGAGAGGCGCGCAGGACGACGCTGTGAGAGCTGAGAGAGAGAGAGGCGCTGC 915
Db      822  CCATGAGAGAGGCGCGCTGAGGACGACGCTGTGAGAGCTGAGAGAGAGAGAGGAGATTGT 881
QY      916  TCCAGGCGCGGAGTGAAGAGTGTGAGGCGCTCGTCCAGAGAGGAGAGCTGACAGAGACA 975
Db      882  TCCAGGCGCGGAGTGAAGAGTGTGAGGCGCTCGTCCAGAGAGGAGAGCTGACAGAGATA 941
QY      976  GCGCTTACATCAAGTACTGAGAGAGAGTGTGCGGCGGCGCTGCGGAGACCAACAGAGAC 1035
Db      942  GCGCATACATCAAGGTGTGAGAGAGAGTGTGCGTCAAGGCACTGAGAGAACACAGAGAGC 1001
QY      1036  AGGCAACACATCTTCTCTCCCTGCGGAGAGAGCTCCGCGAGGCGAGGCCCAAGCGCTCC 1095

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Db 1002 AGCCAGCACCATTCTTCTCCCTACGAAGACCTCCGACGCTGAGGCTCCCGACCC 1061
QY 1096 GGTGATGAGAGAGAGATGTTTCAGCTGACCTGACCTGCACTAGTAAAGATCCA 1155
Db 1062 GGTGATGAGAGAGAGATGTTTCAGCTGACCTGACCTGCACTAGTAAAGATCCA 1121
QY 1156 AGATGTAACAAGACCGCATGAGAGCATCTGCTGCAATGAGAGAGTCCCATTTAGC 1215
Db 1122 AGATGTAACAAGACCGCATGAGAGCATCTGCTGCAATGAGAGAGTCCCATTTAGC 1181
QY 1216 GGGACCAAGACACAAATGAGAGGAGCTGACCACTCCGCGCCAGCGGCTTACGT 1275
Db 1182 GGGAC----- 1186
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QY 1336 CCTCACTGAGGCTCGGCTTGTCTGCTCCCTGACGAGCAATAGCCAGCGGAGAGACTG 1395
Db 1187 -----CAGGCTATGACCTCAAGGAGAGCTG 1213
QY 1396 CACGCAACGACCGCCGCGGCTGCAAGAGAGAGCGCTGCGCAAGAGGTGCGGAG 1455
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QY 1456 CTGGGAGAGAGCGGATGAGCTGACGCTGACAGCTTTCAGAGTGAAGCGAGCTACTG 1515
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QY 1516 GCGCTGAGAGGAGGCTCAGGCGGCGGAGAGCTGCACTCCCGGAGAGCT--GAGAGC 1575
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QY 1576 GAAGATGCTCAACCGAGAGCTCCAGAGCTTCACTCCCGGAGAGCT--GAGAGC 1632
Db 1394 GAAGAGAGTTCCTCCGAGAGCTCCAGAGAGCTTTCAGAGCTGAGAGAGT 1453
QY 1633 ACCGAGCTTCAAGCAAAAGGCTGCTGCGGCGGAGAGCGGAGAGAGAGCTTTTGA 1692
Db 1454 GCCAGCTTCAAGCAAAAGGCTGCTGCGGAGAGAGCGGAGAGAGAGCTTTTGA 1513
QY 1693 GCTCTGACAGAGAGGTTTTCGGAACCCCAATGAGCGAGCTGAGAGCGGAGAG 1752
Db 1514 GTTCTGAACAAGAGGCTTTCGAGAG--CCCATGACAGGCTGCGAGAGAG 1570
QY 1753 CCGCCGAGAGAGCGGCGGCTTCAAGAGAGTTTGAAGACTTCCGAGAGAGAG 1812
Db 1571 CCGCCGAGAGAGCGGCGGCTTCAAGAGAGCTTCAAGAGAGAGAGAGAGAG 1630
QY 1813 GCGCTGAGAGAGTCAAGAGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1872
Db 1631 GCGCTGAGAGAGTCAAGAGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1690
QY 1873 GCGAGGAG 1932
Db 1691 GCGAGGAG 1750
QY 1933 TGACTTGGCTGAGAG 1949
Db 1751 GTTAATGTGAAGGAGATG 1767

RESULT 9
AX154564 1608 bp DNA linear PAT 22-JUN-2001
LOCUS AX154564
DEFINITION Sequence 3 from Patent WO0140468.
ACCESSION AX154564
VERSION AX154564.1 GI:14536157
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
1
AUTHORS Bertin, J.
TITLE Molecules of the card-related protein family and uses thereof
JOURNAL Patent: WO 0140468-A 3 07-JUN-2001;
Milleium Pharmaceuticals, Inc. (US)
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source 1..1608
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
BASE COUNT 407 a 435 c 514 g 252 t
ORIGIN

Query Match 48.0%; Score 1045; DB 6; Length 1608;
Best Local Similarity 77.9%; Pred. No. 1.6e-144;
Matches 1370; Conservative 0; Mismatches 235; Indels 154; Gaps 3;
QY 147 ATGTGAGACTACGAGAGAGATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 206
Db 1 ATGTGAGACTATGAGAGAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 60
QY 207 CTACCTGCTGATGAG 266
Db 61 CTAACTCTGCTGATGAG 120
QY 267 AACCTGATGATGAG 326
Db 121 AACCCGATGATGAG 180
QY 327 GAGGAGTGTCTGAG 386
Db 181 GAGGAGTGTCTGAG 240
QY 387 GAGAGCTGAG 446
Db 241 GAGAGCTGAG 300
QY 447 GCGGCTTCTGATGAG 506
Db 301 GCGGCTTCTGATGAG 360
QY 507 ACTGAGCTGAG 566
Db 361 ACAGAGCTGAG 420
QY 567 GATGAGCTTCAAG 626
Db 421 GATGAGCTTCAAG 480
QY 627 GTGAG 686
Db 481 GTGAG 540
QY 687 GAGAGCTGAG 746
Db 541 GAGAGCTGAG 600
QY 747 ATGCGAG 806
Db 601 ATGCGAG 660
QY 807 GAG 866
Db 661 GAG 720
QY 867 GCGCCAG 926
Db 721 GCGCCAG 780
QY 927 GTGAG 986

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Db      781 GTGCGAGAGCTGAGGCTCTCCGTGCGAGAGGTAAGTTACACGAGTAATGCCATTCATC 840
Qy      987 CAGTACTGAGAGAGAGCTGCGCGCAGAGCGCTGCGGAGACCAAGAGAGAGCCAAACC 1046
Db      841 CAGGTGCTGAGAGAGAGCTGCGCTGAGGACCTGAGAGAAACCAAGAGAGAGCCAAACC 900
Qy      1047 ATCTTCTCCCTGCGAGAGACCTTCGCGCAGAGGCGAGCCGACGCTCCGCTGCAATGAG 1106
Db      901 ATCTTCTCCCTGAGAAAGAGACCTTCGCGCAGAGGCTGAGGCTCCGCGACCCGCTGCAATGAG 960
Qy      1107 GAGAGAGAGATGTTGCGAGCTGCGAGTGGCTGCGCACTAGTAAAGACTCCAAAGTGTCAAG 1166
Db      961 GAAAGAGAGATGTTGCGAGCTGCGAGTGGCTGCGCAAGTGTCAAG 1020
Qy      1167 GACCGATGAGAGGCTGCGCTGCGCAATGAGAGAGTGGCTGAGAGCGGAGCAGAGC 1226
Db      1021 GACCGATGAGAGGCTGCGCTGCGCAATGAGAGAGTGGCTGAGAGCGGAGCAGAGC----- 1074
Qy      1227 ACACAATGAGAGGCTGAGACAGCTCCGCGCCGACGCGCTTGAAGTCCCGAGCC 1286
Db      1075 ----- 1074
Qy      1287 TCTGCTTGAAGTTGCGCGCGCGCGCGAGGCGCAAGCTTGGGCGCTCATGAG 1346
Db      1075 ----- 1074
Qy      1347 GGTGCGCTTGTGCTGTCCGCTCAGGCTATGACCGCGGAGAGAGTGCACGCAAGCA 1406
Db      1075 -----CAGGCTATGACCTCAAGGAGAGAGTGCATCAAGTG 1112
Qy      1407 CGCGCGCGCGCTGAGAGAGAGAGCGCGCTGCGCAAGAGTGGAGAGTGGCGAGAA 1466
Db      1113 TGCCCAAGCTTTAGAGCAAGATTAAGCTGCGAAGCAGAGTTGAGAACTGAGTGA 1172
Qy      1467 GCGCGATGAGAGCTGAGAGTGTTCAGTGTGAGCGCAGCTACTGCGCTGAGAG 1526
Db      1173 GCGCGAGAGTGTGAGAGTGTTCAGTGTGAGCGCAGAGCGAGTGTGCGCGCTGAGAG 1232
Qy      1527 CAGGCTCAGAGCGAGAGAGTGTGAGAGCTGTGCTGAGCTCGAAGTGAAGTGGCTC 1586
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Qy      1587 ACCCAGAGAGTGTGAGAGCTGTGCTGAGCTGTGCTGAGCTGTGCTGAGCTGTGCT 1643
Db      1293 CCGCAGAGAGTGTGAGAGCTGTGCTGAGCTGTGCTGAGCTGTGCTGAGCTGTGCT 1352
Qy      1644 AGAAGAGAGCTGTGCGCGCGCGCGCGAGAGCGCGAAGCAGCTGTGCACTGTGAGCA 1703
Db      1353 AGAAGAGAGTGTGCTGCGAGAGAGAGCGCGAGAGCGCGCTGTGCTGTGAGCA 1412
Qy      1704 GAGAGAGTGTGCGAGAGCGCGAGCTGTGAGAGCTGTGAGAGCGCGAGAGCGCGCGAGAA 1763
Db      1413 GAGAGAGTGTGCGAGAGCGCGAGCTGTGAGAGCTGTGAGAGCGCGAGAGCGCGCGAGAA 1469
Qy      1764 GAGAGAGTGTGCGAGAGCGCGAGCTGTGAGAGCTGTGAGAGCGCGAGAGCGCGCGAGAA 1823
Db      1470 GAGAGAGTGTGCGAGAGCGCGAGCTGTGAGAGCTGTGAGAGCGCGAGAGCGCGCGAGAA 1529
Qy      1824 GATGAGAGAGTGTGCGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
Db      1530 GATGAGAGAGTGTGCGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589
Qy      1884 CACGAGAGTGTGAGAGCGCTCC 1902
Db      1590 CACGAGAGTGTGAGAGCGCTCC 1608

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RESULT 10
BD150612          765 bp  DNA      linear  PAT 17-JAN-2003
LOCUS             BD150612
DEFINITION        Primer for synthesizing full-length cDNA and use thereof.
ACCESSION         BD150612

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VERSION          BD150612.1 GI:27856370
KEYWORDS         JP 2002191363-A/5455.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
REFERENCE        Ota,T., Iwagai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
AUTHORS          Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE            Primer for synthesizing full-length cDNA and use thereof
JOURNAL          Patent: JP 2002191363-A 5455 09-JUL-2002;
                  HELIX RESEARCH INSTITUTE
COMMENT          OS Homo sapiens (human)
                  PN JP 2002191363-A/5455
                  PD 09-JUL-2002
                  PF 28-JUL-2000 JP 2000280990
                  PI TOSHIO OTA,TAKAO IWAGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KOJI
                  PI SAITO,
                  PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
                  PI KETICHI NAGAI,TETSUJI OTSUKI
                  PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
                  10,
                  PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N5/00,C12N5/00 CC
                  Primer for synthesizing full-length cDNA and use thereof FH Key
                  Location/Qualifiers
FEATURES          FT source 1..765
                  source      Location/Qualifiers
BASE COUNT       160 a 236 c 242 g 123 t 4 others
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Query Match      33.3%; Score 725.4; DB 6; Length 765;
Best Local Similarity 99.0%; Pred. No. 2,2e-97;
Matches 759; Conservative 0; Mismatches 5; Indels 3; Gaps 3;
Qy      1 ATCATCAGAGAGTGCACAGAGCGTCCGCGTCTCTCTCCCTGCGAGAGCGCGGAGAGA 60
Db      1 ATCATCAGAGAGTGCACAGAGCGTCCGCGTCTCTCTCTCCCTGCGAGAGCGCGGAGAGA 60
Qy      61 TCTCCAGAGAGTCCGCGAGAGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db      61 TCTCCAGAGAGTCCGCGAGAGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy      121 AACCCCTCAGCCCTGCTGCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db      121 AACCCCTCAGCCCTGCTGCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Qy      181 AGCTCTGAGAGAGCTTCCGAGTGAAGCTCACTCGGTCAAGCCCTCAAGCCATCAAC 240
Db      181 AGCTCTGAGAGAGCTTCCGAGTGAAGCTCACTCGGTCAAGCCCTCAAGCCATCAAC 240
Qy      241 CTTACCTGCGAGAGTGCAGAGTCTGAACCTGATGATGAGAGAGAGAGAGAGAGAGAGAG 300
Db      241 CTTACCTGCGAGAGTGCAGAGTCTGAACCTGATGATGAGAGAGAGAGAGAGAGAGAGAG 300
Qy      301 CCAACTGTGATCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db      301 CCAACTGTGATCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy      361 GCCACAAGAGAGTACAGTGTGCTTCTGAGAGCTGAGAGCTTCACTACCGCAGCTGTACA 420
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Qy      421 AGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db      421 AGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      481 AGTCAGAGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

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Db      481 AGTCAGAGCTGACTGAGCTGATGATGAGTCTGAGTCAAGTCAAGAAAGAGGTCAGAG 540
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Qy      601 GCCTGCTGCGCAAGACCAAGAGCTGTGACAGAGCTCAAGAGAGAGTGCAGAGCGCGCA 660
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Qy      661 GCCGCGAGCTCAAGCGCTGCAAGAGAGAACTAGCACTTGCCATGCGCTTGGCGCAC 720
Db      661 GCCGCGAGCTCAAGCGCTGCAAGAGAGAACTAGCACTTGCCATGCGCTTGGCGCAC 718
Qy      721 AGAGTAGAGAGAGAGGCGCGCGCCGCTCATGCGGAAACCGTGAAGCTGCA 766
Db      719 AATATGAGAGAGAGGCGCGCGCGCTTCATGCGGAAACCGTGAAGCTGCA 765

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RESULT 11
BD155532/c 413 bp DNA linear PAT 17-JUN-2003
LOCUS      Primer for synthesizing full-length cDNA and use thereof.
DEFINITION
ACCESSION  BD155532
VERSION     BD155532.1 GI:27861290
KEYWORDS   UP 2002191363-A/10375.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE 1 (bases 1 to 413)
AUTHORS   Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
           Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE      Primer for synthesizing full-length cDNA and use thereof
JOURNAL    Patent: JP 2002191363-A 10375 09-JUL-2002;
           HELIX RESEARCH INSTITUTE

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COMMENT

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OS Homo sapiens (human)
PN JP 2002191363-A/10375
PD 09-JUL-2002
PF 28-JUL-2000 JP 20002800990
PI TOSHIO OCA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KIORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
PC 10', C12P21/02, C12P1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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BASE COUNT 71 a 120 c 114 g 101 t 7 others
ORIGIN

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Query Match 18.3%; Score 398; DB 6; Length 413;
Best Local Similarity 97.1%; Pred. No. 4.3e-49;
Matches 401; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      1824 GATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
Db      353 GATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294

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Qy      1944 GGAACGAGAGAGTGTGGTCCCTGAAAGGCCAGCCGAGACTGCGGAGGATTTGGGCGCTTT 2003
Db      233 GGAACGAGAGAGTGTGGTCCCTGAAAGGCCAGCCGAGACTGCGGAGGATTTGGGCGCTTT 174
Qy      2004 GTTAAGCGGACACTATTTTGGGAGGCGCATGCGGCTCTACCAACCCCATGACAGCGC 2063
Db      173 GTTAAGCGGACACTATTTTGGGAGGCGCATGCGGCTCTACCAACCCCATGACAGCGC 114
Qy      2064 ATCTGTGTAAGTCAAGATCTGTTCTGTTTCAACATGTAACACAAATATGATGAT 2123
Db      1143 ATCTGTGTAAGTCAAGATCTGTTCTGTTTCAACATGTAACACAAATATGATGATCAT 54
Qy      2124 TGTATTAGTGTAAAGAACAGAGTGGGTAAATTAACAGACGGGTGACCCGC 2176
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RESULT 12
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LOCUS      Human DNA sequence from clone Rp11-413M3 on chromosome 9, complete
DEFINITION
ACCESSION  AL592301
VERSION     AL592301.14 GI:19031459
KEYWORDS   HTG.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE 1 (bases 1 to 189462)
AUTHORS   Dunn,M.
TITLE      Direct Submission
JOURNAL    Submitted (27-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
           Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
           humquerry@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
           On Feb 28, 2002 this sequence version replaced g1:18135088.
           During sequence assembly data is compared from overlapping clones.
           Where differences are found these are annotated as variations
           together with a note of the overlapping clone name. Note that the
           variation annotation may not be found in the sequence submission
           corresponding to the overlapping clone, as we submit sequences with
           only a small overlap as described above.

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COMMENT

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Information on the WormPeP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone configs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9> RP11-413M3 is from the library RP11-11.2 constructed by the group of Plier de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

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FEATURES
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BASE COUNT 40785 a
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Query Match 17.9%; Score 389.8; DB 9; Length 188462;
Best Local Similarity 72.8%; Pred. No. 2.4e-48;
Matches 643; Conservative 0; Mismatches 17; Indels 223; Gaps 2;
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DB 14661 TCAAGAGCTGCGCGGTGAAGAGACACCTGCTGCGACAGACACAGACCGCTGTGACAGAGC 14602
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DB 14541 ACCTGGCCATCGCGCTGCGGACACACAGAGTGAAGAGAGGCGCGCTCATGCGGAAAC 14482
QY 757 GTGACCTGACAGCTG----- 771
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DB 14361 TGAAGGGAACAGACAGGCTCACTGACACTTCTGCAAGATTGACAGCTCAAGCACAGCTTC 14302
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ACCESSION AB086061
VERSION AB086061.1 GI:21326822
KEYWORDS
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
Kono,T., Sakai,T. and Sakai,M.
Molecular cloning and expression analysis of a novel caspase
recruitment domain protein (CARD) in common carp Cyprinus carpio L
Gene 309, 57-64 (2003)
2 (bases 1 to 2031)
AUTHORS Sakai,M. and Kono,T.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-2002) Masahiro Sakai, Miyazaki University,
Faculty of Agriculture, Gakuen kibandai nishi 1-1, Miyazaki,
Miyazaki 889-2192, Japan [E-mail:m.sakai@cc.miyazaki-u.ac.jp,
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REFERENCE		Pomerantz,J.L., Denny,E.M. and Baltimore,D.		
AUTHORS		(bases 1 to 4085)		
TITLE		CARD1 mediates factor-specific activation of NF-kappaB by the T cell receptor complex		
JOURNAL		EMBO J. 21 (19), 5184-5194 (2002)		
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AUTHORS		Pomerantz,J.L., Denny,E.M. and Baltimore,D.		
TITLE		Direct Submission		
JOURNAL		Submitted (23-JUL-2002) Biology, California Institute of Technology, MC 147-75, 1200 E. California Blvd., Pasadena, CA 91125, USA		
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 1 Bertin, J.
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GenCore version 5.1.6
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40	100.6	4.6	1926	22	AAF82902 EBY tethering prot
41	100.6	4.6	2580	21	AA47454 Nucleotide sequenc
42	100.6	4.6	2580	24	AA164275 Epstein-Barr virus
43	100.6	4.6	5452	20	AA590923 Anti-sense strand
44	100.6	4.6	8705	20	AAZ23778 Vector phuntle DN
45	100.6	4.6	9600	19	AAV21683 Vector plasmid pcm

ALIGNMENTS

RESULT 1	AAH18321	standard; cDNA; 2176 BP.
ID	AAH18321	
AC	AAH18321;	
XX		
DT	26-JUN-2001 (first entry)	
XX		
DE	Human cDNA sequence SEQ ID NO:18327.	
XX		
KW	Human; primer; detection; diagnosis; antisense therapy; Gene therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1074617-A2.	
XX		
PD	07-FEB-2001.	
XX		
PF	28-JUL-2000; 2000EP-0116:26.	
XX		
PR	29-JUL-1999; 99JP-0248036.	
PR	27-AUG-1999; 99JP-0300253.	
PR	11-JAN-2000; 2000JP-0118776.	
PR	02-MAY-2000; 2000JP-0183767.	
PR	09-JUN-2000; 2000JP-0241899.	
XX		
PA	(HELT-) HELIX RES INST.	
XX		
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;	
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;	

DR WPI; 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 18327; 2537pp + CD ROM; English.
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2176 BP; 464 A; 657 C; 734 G; 321 T; 0 other;
Query Match 100.0%; Score 2176; DB 22; Length 2176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCATCAGGAAGTGCACAGGCGTCCGCGTCTCTCCCTCCCTGACGCCCGGAGCA 60
Db 1 ATCATCAGGAAGTGCACAGGCGTCCGCGTCTCTCTCTCTCCCTGACGCCCGGAGCA 60
QY 61 TCTCCAGAGGCTCCGCGGCCAGAGCTCTGTGTGTCTGAGTGCAGTGGCTCTGGA 120
Db 61 TCTCCAGAGGCTCCGCGGCCAGAGCTCTGTGTGTCTGAGTGCAGTGGCTCTGGA 120
QY 121 AGACCTCTACGCTGCTGCTGCTGAGGCACTGTGCACTGAGAACATGAGAGAGTGGTGA 180
Db 121 AGACCTCTACGCTGCTGCTGAGGCACTGTGCACTGAGAACATGAGAGAGTGGTGA 180
QY 181 AGCGCTCAGAGGCTCCGCGGTGAAGCTCATCGATGATGACCCCTCAGCATCAC 240
Db 181 AGCGCTCAGAGGCTCCGCGGTGAAGCTCATCGATGATGACCCCTCAGCATCAC 240
QY 241 CTTAAGTCCGAGTGCAGGCTGCTGAACCTGTATGATGAGAGCAGAGTGTGACGACC 300
Db 241 CTTAAGTCCGAGTGCAGGCTGCTGAACCTGTATGATGAGAGCAGAGTGTGACGACC 300
QY 301 CCAACTCTGATCCGCAAGAGTGGTGTGCTCTGAGACATCTCTGACGAGCCG 360
Db 301 CCAACTCTGATCCGCAAGAGTGGTGTGCTCTGAGACATCTCTGACGAGCCG 360
QY 361 GCCACAGAGGCTACGTGGCTTCTCTCAGAGCTTGAGCTCTATACCCGAGTGAACA 420
Db 361 GCCACAGAGGCTACGTGGCTTCTCTCAGAGCTTGAGCTCTATACCCGAGTGAACA 420
QY 421 AGAAGTCAAGGAGGAGGAGCGGCGCGCTTCTCATGATCATGACGCTCCGAGG 480
Db 421 AGAAGTCAAGGAGGAGGAGCGGCGCGCTTCTCATGATCATGACGCTCCGAGG 480
QY 481 AGTCAGGCTGACTCAGCTGTGTGATGATGAGATCATGAGCTGACAGAGAGTGGACG 540
Db 481 AGTCAGGCTGACTCAGCTGTGTGATGATGAGATCATGAGCTGACAGAGAGTGGACG 540

QY 541 ACTGACCGCGCTGCTGAGCTCCAAAGTACCTTCATCAAGAGACTCGGGTGAAGACA 600
Db 541 ACTGACCGCGCTGCTGAGCTCCAAAGTACCTTCATCAAGAGACTCGGGTGAAGACA 600
QY 601 GCTGTGCGCAAGACCAAGAGCGTGTGCAAGAGCTTCAGAGAGAGTGCAGGCGGCA 660
Db 601 GCTGTGCGCAAGACCAAGAGCGTGTGCAAGAGCTTCAGAGAGAGTGCAGGCGGCA 660
QY 661 GCCCGGAGACTCAAGCTGCTGCAAGAGAGAACTTCAGACCTGCGCATGGCGGACCG 720
Db 661 GCCCGGAGACTCAAGCTGCTGCAAGAGAGAACTTCAGACCTGCGCATGGCGGACCG 720
QY 721 AGAGTGAAGAGAGAGGCGCGCGCTCATGCGGAACCGTACCTGACGTGAGATTGACC 780
Db 721 AGAGTGAAGAGAGAGGCGCGCGCTCATGCGGAACCGTACCTGACGTGAGATTGACC 780
QY 781 AGCTCAGACAGAGCTCTCATGAGAGCGCGAGCACTGCAAGGTGAGCGCAAGCAAGC 840
Db 781 AGCTCAGACAGAGCTCTCATGAGAGCGCGAGCACTGCAAGGTGAGCGCAAGCAAGC 840
QY 841 TGAAGCTGAGGACCGCATGAGAGAGCGGCCCAAGCAAGCTGCTGTGGAGCTGACG 900
Db 841 TGAAGCTGAGGACCGCATGAGAGAGCGGCCCAAGCAAGCTGCTGTGGAGCTGACG 900
QY 901 AGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 AGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 AGCTGAGACAG 1020
Db 961 AGCTGAGACAG 1020
QY 1021 GGAACCAACAG 1080
Db 1021 GGAACCAACAG 1080
QY 1081 AGGCGGAG 1140
Db 1081 AGGCGGAG 1140
QY 1141 TACGTAAAGATCTCCAAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 TACGTAAAGATCTCCAAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 AGGTGCGCATTTAG 1260
Db 1201 AGGTGCGCATTTAG 1260
QY 1261 CCAGCGGCTTGAAGTCTCCGAGAGCTTGTGAGAGTGGAGGCGGCGGAGAGAGAG 1320
Db 1261 CCAGCGGCTTGAAGTCTCCGAGAGCTTGTGAGAGTGGAGGCGGCGGAGAGAGAG 1320
QY 1321 AGGCGAAGCTTGGAGGCTTCACTGAGAGGCTTGTGAGAGTGGAGGCTTGTGAGAG 1380
Db 1321 AGGCGAAGCTTGGAGGCTTCACTGAGAGGCTTGTGAGAGTGGAGGCTTGTGAGAG 1380
QY 1381 AGCGGAG 1440
Db 1381 AGCGGAG 1440
QY 1441 AAGCAGAGTGGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAGCAGAGTGGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 GAGGCGAGCTACGTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 GAGGCGAGCTACGTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 CTGAGCTCCGAGCTTGAAGATGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 CTGAGCTCCGAGCTTGAAGATGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620

QY 1621 GACCTGAGGACACCCAGCTCTCAGACAAAGGCTGCTTCCGCGCGGCGGAGACCCGAAA 1680
 DB 1621 GACCTGAGGACACCCAGCTCTCAGACAAAGGCTGCTTCCGCGCGGCGGAGACCCGAAA 1680
 QY 1681 CAGGCTTTGACAGTCTGCACACGAGACAGGTTTGGGAAACCCCAAGAGTTTGAAGACTAC 1740
 DB 1681 CAGGCTTTGACAGTCTGCACACGAGACAGGTTTGGGAAACCCCAAGAGTTTGAAGACTAC 1740
 QY 1741 AGCAGCGGAGAGCGCGCCGAGAGAGAGCGGCGCTCAAGAGAGTTTGAAGACTAC 1800
 DB 1741 AGCAGCGGAGAGCGCGCCGAGAGAGAGCGGCGCTCAAGAGAGTTTGAAGACTAC 1800
 QY 1801 CGCAGAGAGCGCGCCCTCAGAGAGAGTGAAGAGATGCGGAGAGCGGAGAGAGCGG 1860
 DB 1801 CGCAGAGAGCGCGCCCTCAGAGAGAGTGAAGAGATGCGGAGAGCGGAGAGAGCGG 1860
 QY 1861 GAGAAACACACGAGGAGAGACACACGAGACCTGAGGCTCTAGCCGACGAGACTTCC 1920
 DB 1861 GAGAAACACACGAGGAGAGACACACGAGACCTGAGGCTCTAGCCGACGAGACTTCC 1920
 QY 1921 CCGAGCGGCTGCTGACCTTGGGCTGGAAGAGAACTGCGCTGAAAGGCGGAGCGG 1980
 DB 1921 CCGAGCGGCTGCTGACCTTGGGCTGGAAGAGAACTGCGCTGAAAGGCGGAGCGG 1980
 QY 1981 ACTGCGGAGATGGGCGCGCTTGTAAAGCGGACCTATTGCGAGGCGGAGCGG 2040
 DB 1981 ACTGCGGAGATGGGCGCGCTTGTAAAGCGGACCTATTGCGAGGCGGAGCGG 2040
 QY 2041 CTCACACCCCGACGACGAGCCATCTGTGTAACCTGAGATCTGTTTCAACATG 2100
 DB 2041 CTCACACCCCGACGACGAGCCATCTGTGTAACCTGAGATCTGTTTCAACATG 2100
 QY 2101 TAACACCAATACATGATGATGTTTAAAGAAACACAGCTGCGTAAATTAAC 2160
 DB 2101 TAACACCAATACATGATGATGTTTAAAGAAACACAGCTGCGTAAATTAAC 2160
 QY 2161 AGCAGCGGATGACCCG 2176
 DB 2161 AGCAGCGGATGACCCG 2176

RESULT 2
 ID ABL1432 standard; DNA; 2176 BP.
 XX ABL1432;
 XX
 DT 09-MAY-2003 (first entry)
 XX
 XX DNA encoding caspase recruitment domain containing protein, CARD-10X.
 XX
 KW CARD; caspase recruitment domain; cancer; glioma; carcinoma; adenocarcinoma;
 KW cytokine receptor signaling; apoptosis; cell adhesion; inflammation;
 KW CARD-containing polypeptide associated disorder; sarcoma; melanoma; ds;
 KW hamatoma; leukemia; lymphoma; keratinocyte hyperplasia; neoplasia;
 KW keloid; benign prostatic hyperplasia; inflammatory hyperplasia; fibrosis;
 KW restenosis; allergy; arthritis; lupus; Sjogren's syndrome; sepsis; gene;
 KW Crohn's disease; ulcerative colitis; graft versus host disease; stroke;
 KW abnormal cell death disease; myocardial infarction; heart failure;
 KW neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV;
 KW CARD-10X; caspase activator; caspase inhibitor.
 XX
 XX OS
 XX Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 147..1247
 FT /tag= a
 FT /product= "CARD-10X"
 FT /tag= b
 FT /note= "Encodes caspase recruitment domain (CARD).
 FT Specifically claimed in claim 2"
 FT misc_feature 606..1037

FT /tag= c
 FT /note= "Encodes filament domain. Specifically claimed in
 FT claim 2"
 XX
 XX US2002164703-A1.
 XX
 XX 07-NOV-2002.
 XX
 XX 19-DEC-2001; 2001US-0032159.
 XX
 XX 21-DEC-2000; 2000US-257457P.
 XX
 XX (PAWL/) PAWLOWSKI K.
 XX (REED/) REED J C.
 XX (GODZ/) GODZIK A.
 XX
 XX Pawlowski K, Reed JC, Godzik A;
 XX
 XX MPI; 2003-288137/28.
 XX P-PSDB; A8676060.
 XX
 XX New isolated CARD-containing nucleic acids, useful for the diagnosis
 XX and treatment of disorders with aberrant expression or activity of the
 XX CARD-containing polypeptide, such as cancer, stroke, arthritis, heart
 XX failure and AIDS
 XX
 XX Disclosure; Fig 4; 34pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule encoding a
 XX caspase recruitment domain (CARD) containing polypeptide. CARD containing
 XX polypeptides are involved in apoptosis (as caspase activators and caspase
 XX inhibitors), cell adhesion, inflammation and cytokine receptor
 XX signaling. The methods and compositions of the present invention are
 XX useful for the diagnosis and treatment of disorders associated with the
 XX aberrant expression or activity of the CARD containing polypeptide such
 XX as cancer, glioma, carcinoma, adenocarcinoma, sarcoma, melanoma, keloid,
 XX hamatoma, leukemia, lymphoma, keratinocyte hyperplasia, neoplasia,
 XX benign prostatic hyperplasia, inflammatory hyperplasia, fibrosis,
 XX restenosis, allergies, inflammatory diseases such as arthritis, lupus,
 XX Sjogren's syndrome, Crohn's disease, ulcerative colitis, graft versus
 XX host disease, sepsis, abnormal cell death diseases such as stroke,
 XX myocardial infarction, heart failure, neurodegenerative diseases like
 XX Parkinson's disease and Alzheimer's disease, and HIV infection. The
 XX present sequence represents DNA encoding the caspase recruitment domain
 XX containing protein, CARD-10X.
 XX
 XX Sequence 2176 BP; 464 A; 657 C; 734 G; 321 T; 0 other;
 XX
 XX Query Match 100.0%; Score 2176; DB 25; Length 2176;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 2176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATCATAGGAGATGACAGAGGCTCCGGGATGCTCCCTCCCTGAGGCCCGGAGACA 60
 DB 1 ATCATAGGAGATGACAGAGGCTCCGGGATGCTCCCTCCCTGAGGCCCGGAGACA 60
 QY 61 TCTCCAGAGAGCTCCGCGGCCAGAGCTCTGATGTTGACAGTGAAGTGAAGTCTCTGA 120
 DB 61 TCTCCAGAGAGCTCCGCGGCCAGAGCTCTGATGTTGACAGTGAAGTGAAGTCTCTGA 120
 QY 121 AGACCTGAGCTGCTGCTGAGGCGCATGTCGAGTACAGAAAGCATGACGAGTCTGA 180
 DB 121 AGACCTGAGCTGCTGCTGAGGCGCATGTCGAGTACAGAAAGCATGACGAGTCTGA 180
 QY 181 AGCTCTGAGAGGCTTCCGGGTGAGCGCTACCTCGGTATGACCCCTAAGCATACAC 240
 DB 181 AGCTCTGAGAGGCTTCCGGGTGAGCGCTACCTCGGTATGACCCCTAAGCATACAC 240
 QY 241 CTTACCTGCGGAGATGACAGATCTGAACTGATGATGAGAGAGAGTCTCAGAGACC 300
 DB 241 CTTACCTGCGGAGATGACAGATCTGAACTGATGATGAGAGAGAGTCTCAGAGACC 300
 QY 301 CCAACTGTGATCCGCAACGAAAGTGTGTGTCTCTGACATCTGACGCGGACCG 360


```

Db      |||||
301  CCAACCTGGTCAATCCGGAAGGAAAGTGGTGTGCTCGTGAACATCTGACAGGACCG 360
Qy      |||||
361  GCCACAAAGGCTACGTGGCTTCTCTGAGAGCTTGAAGCTCTTACCTCCAGCTGTACA 420
Db      |||||
361  GCCACAAAGGCTACGTGGCTTCTCTGAGAGCTTGAAGCTCTTACCTCCAGCTGTACA 420
Qy      |||||
421  AGAAGGTCAAGGGAAGGACCGGCGCTTCTTCATGATCATTCAGAGCGGTCCGGGG 480
Db      |||||
421  AGAAGGTCAAGGGAAGGACCGGCGCTTCTTCATGATCATTCAGAGCGGTCCGGGG 480
Qy      |||||
481  AGTCAAGCTGATCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db      |||||
481  AGTCAAGCTGATCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy      |||||
541  ACCTGACCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db      |||||
541  ACCTGACCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Qy      |||||
601  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      |||||
601  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy      |||||
661  GCGCGAGCTCAAGCGCTGCAAGGAGGAACTACGACCTGCGCATGCGCTGCGCAC 720
Db      |||||
661  GCGCGAGCTCAAGCGCTGCAAGGAGGAACTACGACCTGCGCATGCGCTGCGCAC 720
Qy      |||||
721  AGAAGTGAAGAGAGGCGCGCTCATGCGGAACTGATGATGATGATGATGATGATGAT 780
Db      |||||
721  AGAAGTGAAGAGAGGCGCGCTCATGCGGAACTGATGATGATGATGATGATGATGAT 780
Qy      |||||
781  AGCTCAAGCAAGCTCTATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db      |||||
781  AGCTCAAGCAAGCTCTATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Qy      |||||
841  TGAAGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db      |||||
841  TGAAGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Qy      |||||
901  AGAAGAGGCGCTCTCAAGGCGCGGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db      |||||
901  AGAAGAGGCGCTCTCAAGGCGCGGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy      |||||
961  AGCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Db      |||||
961  AGCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Qy      |||||
1021  GGAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db      |||||
1021  GGAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Qy      |||||
1081  AGGAGCGAGCGCTCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Db      |||||
1081  AGGAGCGAGCGCTCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Qy      |||||
1141  TAGGTAAAGAGCTCAAGATGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db      |||||
1141  TAGGTAAAGAGCTCAAGATGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Qy      |||||
1201  AGGTGCGCATTTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Db      |||||
1201  AGGTGCGCATTTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Qy      |||||
1261  CCAAGCGGCTTGAAGCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db      |||||
1261  CCAAGCGGCTTGAAGCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Qy      |||||
1321  AGGAGCAAGCTTGGGCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db      |||||
1321  AGGAGCAAGCTTGGGCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Qy      |||||
1381  AGGAGCAAGCTTGGGCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440

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Db      |||||
1381  ACAGCGAGGAGGAGCTGCAAGCAAGCAAGCGCGGAGCTGCAAGGAGGAGGAGGAGG 1440
Qy      |||||
1441  AAGAGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
Db      |||||
1441  AAGAGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
Qy      |||||
1501  GAGGCGAGCTTACGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db      |||||
1501  GAGGCGAGCTTACGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Qy      |||||
1561  CTGAGCTCGAAGCTTGAAGATGCTCAACCAAGAGGAGGAGGAGGAGGAGGAGGAG 1620
Db      |||||
1561  CTGAGCTCGAAGCTTGAAGATGCTCAACCAAGAGGAGGAGGAGGAGGAGGAGGAG 1620
Qy      |||||
1621  GACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Db      |||||
1621  GACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Qy      |||||
1681  GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
Db      |||||
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Qy      |||||
1741  AGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
Db      |||||
1741  AGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
Qy      |||||
1801  CGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
Db      |||||
1801  CGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
Qy      |||||
1861  GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Db      |||||
1861  GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Qy      |||||
1921  CCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Db      |||||
1921  CCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Qy      |||||
1981  ACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Db      |||||
1981  ACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Qy      |||||
2041  CTACACACCCCATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Db      |||||
2041  CTACACACCCCATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Qy      |||||
2101  TAAACACAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Db      |||||
2101  TAAACACAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Qy      |||||
2161  AGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
Db      |||||
2161  AGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220

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RESULT 3

AA05387
ID AA05387 standard, cDNA, 2098 BP.

AA05387;

12-SEP-2001 (first entry)

Human caspase recruitment domain, CARD-9 cDNA sequence.

Human; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB;

apoptosis; hyperproliferative disorder; autoimmune; neurological;

inflammatory disorder; viral infection; stress-related response; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 144..1754

Db	1218	-----CAGGCCATAGCCACGCGGGAGAGCTGCACG	1253
QY	1405	CAGCCCTCGGCGCTTGCAGAGGAAAGACGCGCTGCGAA	1464
Db	1254	CAGCCCTCGGCGCTTGCAGAGGAAAGACGCGCTGCGAA	1313
QY	1465	AAGCGGATAGAGCTGCAGCTGCAGGTGTTCCAGGTGAG	1524
Db	1314	AAGCGGATAGAGCTGCAGCTGCAGGTGTTCCAGGTGAG	1373
QY	1525	GCGAGGCTCAGCGCGGCAAGCTGGAACGCTCGTCTGAG	1584
Db	1374	GCGAGGCTCAGCGCGGCAAGCTGGAACGCTCGTCTGAG	1433
QY	1585	TCACCCAGAGAGTCCAGAGACTTCTACTCCCCAGAGCT	1644
Db	1434	TCACCCAGAGAGTCCAGAGACTTCTACTCCCCAGAGCT	1493
QY	1645	GACAAAGGCTGCGCTTGCAGGCGGAGGAGCCGAAACAG	1704
Db	1494	GACAAAGGCTGCGCTTGCAGGCGGAGGAGCCGAAACAG	1553
QY	1705	GAGCAGGTTTTCGCGAAACCCCATAGACGCAAGCTTGA	1764
Db	1554	GAGCAGGTTTTCGCGAAACCCCATAGACGCAAGCTTGA	1613
QY	1765	GAGCGCGCGCGCTTCAAAGAGAGTTTGGAGACTTAC	1824
Db	1614	GAGCGCGCGCGCTTCAAAGAGAGTTTGGAGACTTAC	1673
QY	1825	ATGCAGAAAGATGCGCGCAGGGGAGAGAACCGGAGAA	1884
Db	1674	ATGCAGAAAGATGCGCGCAGGGGAGAGAACCGGAGAA	1733
QY	1885	ACCGACACTGAGGAGCTCCTAGCCGCA-----	1910
Db	1734	ACCGACACTGAGGAGCTCCTAGCCGCAAGAGCGAGCCCG	1793
QY	1911	-----GCAGACTTCCCGAGCCGTGCT	1933
Db	1794	CCCGGCTGCGCACCGGGGGTGCAGACGCTTGGGGGCG	1853
QY	1934	GACTTGGCTTGGAAACGAGGAATCTGTGTCCCTGAAAG	1993
Db	1854	GACTTGGCTTGGAAACGAGGAATCTGTGTCCCTGAAAG	1913
QY	1994	GGGGCGTTTGTGTTAAGCGGCACTAATTTGCGAGGAGC	2053
Db	1914	GGGGCGTTTGTGTTAAGCGGCACTAATTTGCGAGGAGC	1973
QY	2054	TGCACACGCCACTCTGTGTACTTCAGATCTGTTCTGTT	2113
Db	1974	TGCACACGCCACTCTGTGTACTTCAGATCTGTTCTGTT	2033
QY	2114	ATGCATGCTGTATTAGTGT-AGAAAACACAGCTGGCTAA	2173
Db	2034	ATGCATGCTGTATTAGTGT-AGAAAACACAGCTGGCTAA	2093
QY	2173	COGC 2176	
Db	2094	COGC 2097	

KM	Gene; rat; human; caspase recruitment domain; CARD-9; CARD-10;
KM	CARD-11; apoptosis; inflammation; cell growth; cell death;
KM	lymphocyte activation; cancer; melanoma; autoimmune disease;
KM	arthritis; neurological disorder; Alzheimer's disease; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
CD	144..1754
FT	/tag= a
FT	/product= "CARD-9"
XX	
PN	W0200270652-A2.
PD	12-SEP-2002.
XX	
PF	28-FEB-2002; 2002WO-US06147.
PR	02-MAR-2001; 2001US-0798412.
PA	(MILL-) MILLENNIUM PHARM INC.
PI	Bertin J;
DR	WPI; 2002-698749/75.
PB	P-PDB; AAG79553.
XX	
PT	CARD-9; CARD-10 or CARD-11 polypeptides and polymucleotides, useful for
PT	treating disorders associated with inappropriate apoptosis or
PT	lymphocyte activation, e.g. cancer
XX	-
PS	Disclosure; Fig 5; 151pp; English.
XX	
CC	This sequence encodes human caspase recruitment domain (CARD)-9.
CC	CARD proteins play roles in apoptotic and inflammatory signaling
CC	pathways. CARD-9, -10 and -11 participate in the network of
CC	interactions that modulate caspase activity. They are thought to be
CC	useful as modulating agents for regulating a variety of cellular
CC	processes including cell growth and cell death. CARD proteins and
CC	nucleic acids are useful for treating a disorder associated with
CC	inappropriate apoptosis or lymphocyte activation or for diagnosing
CC	subjects having or that are at risk of developing a disorder associated
CC	with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such
CC	as cancer e.g., melanoma, autoimmune disorders e.g. arthritis, or
CC	neurological disorders e.g. Alzheimer's disease.
XX	
SQ	Sequence 2098 BP; 455 A; 644 C; 702 G; 297 T; 0 other;
Query Match	80.2%; Score 1746; DB 24; Length 2098;
Best Local Similarity	89.9%; Pred. No. 4, 5e-295;
Matches 1999; Conservative	0; Mismatches 5; Indels 220; Gaps 3
OY	CGGCGTGCCTCCTCCCTCGAGGCCGGGACATCTCCAGAGGCTCCGCGCCAG 84
DB	
22	CGTCGGGTCTCTCTCTCTCGAGGCCGGGAGATCTCCAGAGGCTCCGCGCCAG 81
OY	85 GCTCTGTTGTCTGCACTGAGGTGCTCTTGAAAGACCTTAGCTGCTGAGG 144
DB	82 GTCTGTGTTGTCTGCACTGAGGTGCTCTTGAAAGACCTTAGCTGCTGAGG 141
OY	145 CCATTGCGACTACAGAAACCATGACGAGTCTTGAAAGTCTTGAGGGCTTCGGGGTA 204
DB	142 CCATTGCGACTACAGAAACCATGACGAGTCTTGAAAGTCTTGAGGGCTTCGGGGTA 201
OY	205 CGCTACCTCGGTGATCGAGCCCTCACGATCACACTTACTCGGCGAGTGCAGAAGTCC 264
DB	202 CGCTACCTCGGTGATCGAGCCCTCACGATCACACTTACTCGGCGAGTGCAGAAGTCC 261
OY	265 TGAACCTTGATGAGGAGCAGGTCTTACGAGACCCAACTTGATATCGCAACGGA 324
DB	262 TGAACCTTGATGAGGAGCAGGTCTTACGAGACCCAACTTGATATCGCAACGGA 321
OY	325 AAGTGGTGTGCTCTCTGAGCATCTCTGACGCGGACCGGCGAACAGGGCTACGTGGCTTCC 384

Db 322 AAGTGGTGTGCTCTGAGCATCTGACAGCGACCGGCAAAAGGCTACGTGGCTTTC 381
 Qy 385 TCGAGAGCTGAGAGCTCTACTACCCGACAGCTGTACAAGAGGTCAAGGCAAGAGCGG 444
 Db 382 TCGAGAGCTGAGAGCTCTACTACCCGACAGCTGTACAAGAGGTCAAGGCAAGAGCGG 441
 Qy 445 CCGGCTCTTCTCCATGATCATGACGCGTCCGGGAGTCAAGGCTGACTGACTGCTGA 504
 Db 442 CCGGCTCTTCTCCATGATCATGACGCGTCCGGGAGTCAAGGCTGACTGACTGCTGA 501
 Qy 505 TGACTGAGGTCAATGAGCTGACAGAAAGGTGACGACTGACCGGCTGCTGAGTCCA 564
 Db 502 TGACTGAGGTCAATGAGCTGACAGAAAGGTGACGACTGACCGGCTGCTGAGTCCA 561
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 Db 562 AAGATGACTTCAATCAAGAGCTGCGGGTGAAGGACGCTGCTGCGCAAGCAAGAGAGC 621
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 Db 622 GTGTGCAAGAGCTCAAGAGAGTGGAGGCGGACGCGGAGCTCAAGCGCTGCAAG 681
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 Db 682 AGAGGAACTACGACTGAGCCATGCGCTGGCGCAACAAGTGAAGAAAGGCGCGCGC 741
 Qy 745 TCATGCGGAACCGTGAATCTGACCTGAGCTGAGATTGACCAAGCTCAAGCTCATATAAG 804
 Db 742 TCATGCGGAACCGTGAATCTGACCTGAGATTGACCAAGCTCAAGCTCATATAAG 801
 Qy 805 CCGAGAGACGACTGCAAGTGGAGCGACAGACAAGCTGAAGCTCAAGGCAAGCGATGAGC 864
 Db 802 CCGAGAGACGACTGCAAGTGGAGCGACAGACAAGCTGAAGCTCAAGGCAAGCGATGAGC 861
 Qy 865 AGGAGCCAGACGAGAGCTGCTGGGAGCTGAGCAGAGAGAGGCGCTGCTCAAGCGC 924
 Db 862 AGGAGCCAGACGAGAGCTGCTGGGAGCTGAGCAGAGAGAGGCGCTGCTCAAGCGC 921
 Qy 925 GGGTGCAGAGCTGAGAGCTCCGTCACAGAGGAGGAACTGACAGAGAGAGCGCTTACA 984
 Db 922 GGGTGCAGAGCTGAGAGCTCCGTCACAGAGGAGGAACTGACAGAGAGAGCGCTTACA 981
 Qy 985 TCCAGTACTGAGAGAGAGTGGCGGAGCGCTGCGGAGCAACAGAGAGAGCGCAAC 1044
 Db 982 TCCAGTACTGAGAGAGAGTGGCGGAGCGCTGCGGAGCAACAGAGAGAGCGCAAC 1041
 Qy 1045 CCACTTCTCCCTGCGCAAGAGCTCCGCAAGGCGGAGCGCGCTCCGGTGGATGG 1104
 Db 1042 CCACTTCTCCCTGCGCAAGAGCTCCGCAAGGCGGAGCGCGCTCCGGTGGATGG 1101
 Qy 1105 AGGAGAGAGAGTGTGAGCTGAGTGGCTGGCACTACGTAAGAACTCCAAATGTACA 1164
 Db 1102 AGGAGAGAGAGTGTGAGCTGAGTGGCTGGCACTACGTAAGAACTCCAAATGTACA 1161
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 Db 1218 ----- 1217
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 Db 1218 ----- 1217
 Qy 1345 AGGATCGGCTTGTGCTGTCCGTCAGGCACTAGCCAGCGGAGAGAGCTGACGCAAG 1404
 Db 1218 -----CAGGCCATAGCCAGCGCGGAGAGAGCTGACGCAAG 1253
 Qy 1405 CACGCCCGGAGCTGACAGAGAGAGCGCGTGCAGCAAGAGGTGCGGAGACTGGGCGAG 1464

Db 1254 CACGCCCGGAGCTGACAGAGAGAGAGCGCGCTGCGCAAGAGGTGCGGAGCTGGCGAG 1313
 Qy 1465 AAGGCGATGAGCTGACAGCTGACAGGTGTTCCAGTGTGAGGCGGAGCTTACTGGCTGAG 1524
 Db 1314 AAGGCGATGAGCTGACAGCTGACAGGTGTTCCAGTGTGAGGCGGAGCTTACTGGCTGAG 1373
 Qy 1525 GGCAGGCTCAAGCGGAGAGCTGAGAGCGTGGTCCGAGCTCCGAGCTGGAGAGATGGC 1584
 Db 1374 GGCAGGCTCAAGCGGAGAGCTGAGAGCGTGGTCCGAGCTCCGAGCTGGAGAGATGGC 1433
 Qy 1585 TCACCAGAGAGTCCAGAGAGCTCTCACTCCCCAGAGCCTGAGAGACACCAGCTTCA 1644
 Db 1434 TCACCAGAGAGTCCAGAGAGCTCTCACTCCCCAGAGCCTGAGAGACACCAGCTTCA 1493
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 Db 1494 GACAAAGCTGCTTGGCGGCGGAGAGCGCGAAAGCGCTTTGCAAGCTTGCACACAG 1553
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 Db 1554 GAGCAGTTTTTGGCGAACCCTCATGACGAGGCTGAGCAGCGGAGCGCGCGAGAG 1613
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 Db 1614 GAGCGGCGGCGCTTGAAGAGATTGAGAACTTGAAGAAAGCGCGCTGAGAGAG 1673
 Qy 1825 ATGCAAGAAAGTGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1884
 Db 1674 ATGCAAGAAAGTGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1733
 Qy 1885 ACCGACACTGAGGAGCTCTTACCGCA ----- 1910
 Db 1734 ACCGACACTGAGGAGCTCTTACCGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793
 Qy 1911 -----GAGACTTCCCTGAGCGCT 1933
 Db 1794 CCGGCTGACACCGGAGGAGTGGCGAGCGCTGAGGAGAGAGAGAGAGAGAGAGAG 1853
 Qy 1934 GACTTGGCTGAGAGAGAGATCTGGTGCCTGTAAGAGCGGAGCTGCGGAGAT 1993
 Db 1854 GACTTGGCTGAGAGAGAGATCTGGTGCCTGTAAGAGCGGAGCTGCGGAGAT 1913
 Qy 1994 GGGGCGTTTGTAAAGCGGAGCTCATTTTGGGAGAGCGGAGGAGTGTCAACACCCCA 2053
 Db 1914 GGGGCGTTTGTAAAGCGGAGCTCATTTTGGGAGAGCGGAGGAGTGTCAACACCCCA 1973
 Qy 2054 TGCACAGCGCATCTGTGTAACCTTCAAGATCTGTCTGTTTCAACATGTACACAAATAC 2113
 Db 1974 TGCACAGCGCATCTGTGTAACCTTCAAGATCTGTCTGTTTCAACATGTACACAAATAC 2033
 Qy 2114 ATGATGACTTGTATTAGTGT -AGAAAACAGAGCTGGTAATTAACAGCAGGATAC 2172
 Db 2034 ATGATGACTTGTATTAGTGTAAAGAAAACAGAGCTGGTAATTAACAGCAGGATAC 2093
 Qy 2173 CCGC 2176
 Db 2094 CCGC 2097

RESULT 5

AAS05386 standard; cDNA; 1879 BP.

AAS05386;

12-SEP-2001 (first entry)

Rat caspase recruitment domain, CARD-9 cDNA sequence.

Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB;

apoptosis; hyperproliferative disorder; autoimmune; neurological;

inflammatory disorder; viral infection; stress-related response; ss.

XX	Rattus sp.	
XX	Key	Location/Qualifiers
FT	CDS	113..1723
FT		/tag= a
FT		/product= "CARD-9"
FT		/note= "ORF is specifically claimed"
XX		
XX	MO200140468-A2.	
XX		
PD	07-JUN-2001.	
PF	01-DEC-2000; 2000MO-US32716.	
PR	03-DEC-1999; 99US-0168780.	
PR	18-FEB-2000; 2000US-0507533.	
PR	25-FEB-2000; 2000US-0513904.	
PR	10-OCT-2000; 2000US-0685791.	
PA	(MILL-) MILLENNIUM PHARM INC.	
P1	Bertin J;	
XX		
XX	WPI; 2001-367809/38.	
DR	P-P5DB; AAU01204.	
XX		
PT	Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10,	
PT	CARD-11, useful as targets for therapy, as immunogens, and in screening	
PT	and detection assays -	
XX		
PS	Claim 2; Fig 1A-1B; 145pp; English.	
XX		
CC	The present sequence encoding for novel rat caspase recruitent	
CC	domain, CARD-9 is isolated from a rat neuronal cDNA library. Also	
CC	described are novel human sequences for CARD-9, CARD-10 and CARD-11	
CC	(AAU01205-AAU01207). CARD-9, CARD-10 and CARD-11 interact with Bcl-10	
CC	which is thought to activate nuclear factor (NF)-kappaB and apoptosis.	
CC	The sequences of the invention can be used for treating a disorder	
CC	associated with abnormal levels of apoptosis by modulating the	
CC	expression or activity of CARD-9, CARD-10, or CARD-11. They can be	
CC	used for the treatment of hyperproliferative disorders (e.g. cancer),	
CC	autoimmune disorders (e.g. systemic lupus erythematosus), neurological	
CC	disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g.	
CC	Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide,	
CC	polynucleotide and an antibody which selectively binds to CARD can be	
CC	used in screening and detection assays (e.g. chromosomal mapping, tissue	
CC	titrals), predictive medicine (prognostic assays, monitoring clinical	
CC	trials), and therapy (treatment and prophylaxis). The CARD polypeptide may	
CC	be used to screen for drugs that bind to and/or modulate it. CARD	
CC	sequences are potential targets for regulating inflammation, cancer,	
CC	NF-kappaB signaling, stress-related response and apoptosis in human	
CC	disease. A host cell containing a polynucleotide encoding CARD can be	
CC	used to create transgenic animals.	
XX		
SQ	Sequence 1879 BP; 496 A; 503 C; 578 G; 302 T; 0 other;	
XX		
Query Match	48.7%; Score 1060.2; DB 22; Length 1879;	
Best Local Similarity	76.2%; Pred. No. 1.le-175;	
Matches 131; Conservative	0; Mismatches 288; Indels 158; Gaps	4
QY	76 GGGGCCCCAGGCTTCGTGTGTCTGTGAATGACAGTGTGCTCCCGAAGAACCCTCAGCTGC	135
DB	46 GTGCCCATATGCCCAGGACACATCCACGTGGCAGGTGGCTCCACAGAACCTCGA----GC	101
QY	CTGCTGAGGCGCATGTGTGGACTACAGAAAGATAGACAGTGCTGGAACGTCTGGAGGGCT	195
DB	102 CTACAGAGSACATGTATGACTATGAAAATGACAGCAAGATGTGAGTGGCTCGAGAGCT	161
QY	196 TCCGGGTGACGCTCACCTCGGTATGACCCCTCAGCAGATCACACTTAACCTCGGAGCT	255
DB	162 TCCGGGTGAAGCTAATCTCTGATTTGACCCCTCAGGAATACACCCATAATTGCGCAGT	221
QY	256 GCAGAGTCTGAACCTGTATGATGAGAGCAGGTGCTCAGCAGCCCAACCTGTGTATCTC	315

Db	222	GCAAAGCTCGAAGCCCGAATGATGAGGACAGAGTCTCAGTGAACCCCAACCTGTGTCATCC	281
Qy	316	GCAAACGGAAGTGGGTGTGCTCTGAGACATCTCTGACGAGGACCCGCGCAAAAGGGCTAGG	375
Db	282	GCAAGCGGAAGTGGGTGTGCTCTGAGACATCTCTGACGAGGACAGGCGCAAAAGGGCTTAGG	341
Qy	376	TGGCTCTTCTCGAAGAGCTGAGAGCTTACTACCCGAGCTGTATCAAGAAGTTCACAGGCA	435
Db	342	TGGCTCTTCTTGAAGAGCTGGAACCTTACTACCCCTCAGTTATATACAGGAAGTCACTGGCA	401
Qy	436	AGAAGCCGAGCCGCGTCTTCTCCATGATCATGCAAGAGTTCAGAGGAGTCAAGGCTTGAATC	495
Db	402	AGAAGCCGAGCGGCTGTCTTCTCATGATCATGCAAGCATCAGAGGAGTGGGCTGTGACCG	461
Qy	496	AGCTCTGATGACTGAGAGTCAATGAAGCTGTGAGAAAGAGTTCAGAGGACCTGACCGCGCTGC	555
Db	462	AGCTCTGATGATGAGAGTCAATGAAGCTGTGAGAAAGAGTTCAGAGGACCTGACCGCGCTTTC	521
Qy	556	TGAGCTCCAAAGATGATGATTCATCAAGAGAGTGGGGGTGAAGACACAGCTGTCTCGCAAG	615
Db	522	TGAGCTCCAAAGATGATTCATCAAGAGAGTGAAGGTGAAGACACAGCTCTCTCGCAAG	581
Qy	616	ACCAGAGAGCTGTGTACAGAGGCTCAAGAGAGAGTGTGAGAGCCGAGCAGCTCAAGCTCAAG	675
Db	582	ACCAGAGAGCGGGTTCAGCGGCTCAAGAGAGAGTGTGAGCTGACAGAGTCCGAGCTGAAGC	641
Qy	676	GCTTCAGAGAGAGAGATTAACGACTGTGCTCATGTGGCTGTGGCGCACAGAGTGAAGAGAAAG	735
Db	642	GCTTCAGAGAGATGAGAACTACGACTGTGCTCATGTGGCTGTGACCTGAGTGAAGAGAAAGG	701
Qy	736	GCGCGCGGCTCATGCGGAAACGGTGAACCTTGACGCTGAGATTAACAGCTCAACACAGCC	795
Db	702	GAGACGACTCATGTCGGAACCGTGAACCTTGAGCTTGAAGTGAACAGCTCAAGGACAGCC	761
Qy	796	TCATGAAGAGCCGAGAGACGACTGCAAGGTGAGGCGCAAGCACAGCTGAAGCTTAGGACG	855
Db	762	TCATGAAGAGCGAGAGATGACTGCAAGGTGAGGCGCAAAACACATGAAGCTCCGGACG	821
Qy	856	CCATGAGAGCAGCGGCCCAAGCCAGAGAGTGTCTGTGTGGAGCTTGCACAGCAGAGAAAGGCCCTGC	915
Db	822	CCATGAGAGCAGCGGCTTAGCCAGAGAGCTGTGTGTGGAGCTTGCACAGCAGAGAAAGGAGACTTGT	881
Qy	916	TCCAGGCCCCGGGTTCAGAGAGCTGAGAGGCCCTCCGTCAGAGAGGGGAAGCTGACAGAGCA	975
Db	882	TGCAGGCCCCGGGTTCAGAGAGCTGAGAGGCTTCCTCGTGCAGAGAGGTTCACACAGGATAT	941
Qy	976	GCCCCATATCAGAGTACTGGAGAGGAGACTGGCGGCGAGGCGCTTCGCGGAACACCCAGAGG	1035
Db	942	GCCCCATATATCAGAGTGTCTGAGAGAGAGACTGGCGGTCAAGGCACTTCAGAGAACACAGAGAG	1001
Qy	1036	AGGCCAACACATTTCTTCCTGTGCAAGGACCTCCGCGCAGAGGCGAGGCCCGGACGCTCC	1095
Db	1002	AGGCCAGACCATTTCTTCCTTCAGAAAGGACCTCCGCGCAGAGGCGAGGCCCTTCGCGAGCC	1061
Qy	1096	GGTGATGAGAGAGAGAGAGATTTTCCAGCTGTGCAAGTCCCTGGCACTTACCTGTAAGACATCCA	1155
Db	1062	GGTGATGAGAGAGAGAGAGATTTTCCAGCTGTGCAAGTGTGCGCTTGGCGCAGAGATGCA	1121
Qy	1156	AGATTTACAAGAACCGCATCGAGGCCCATCTGTGTGAGATGAGAGAGTTCGCCATTGAGC	1215
Db	1122	AGATTTACAAGAACCGGATCGAGGCTATCTGTGCAAGCAGATGAGAGAGTCTCCATTGAGC	1181
Qy	1216	GGGACCAAGACACAAATGAGAGGCGCTGTGACAGGCTCCGCGCCACAGCGGCTTGACGT	1275
Db	1182	GGGAC-----	1186
Qy	1276	CCTCCGAGGCTCTGTCTTGAAGTGGGCGGCGCGGCGCAAGGCGCCAGGCGCAAGCTTGGG	1335
Db	1187	-----	1186
Qy	1336	CCCTACTGAGGGTGGGCTGTGTCTGTCCGTCAGGCAATAGCCAGCGGAGAGAGCTG	1395

Db 1187 -----CAGGTATGACCTCAAGGAAGAGCTG 1213
 QY 1396 CACGACAGACAGCCCGGGGCTGAGAGAGAGACCGGCTGCCAGACAGAGTCCGGAG 1455
 Db 1214 CATGACAGTGTGTCCCAAGCTTTCAGGACAAAGTAAGTCCGAAAGCAGATTGAGAA 1273
 QY 1456 CTGGGCGAAGAGCGGATGAGTGTGAGAGTGTCCAGTGTGAGAGCGCAGCTCTG 1515
 Db 1274 CTGATGAGAGAGCGGACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1333
 QY 1516 GCCGTGAGAGAGCGGCTGAGGCGGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1575
 Db 1334 GCCGTGAGAGAGCGGCTGAGGCGGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1393
 QY 1576 GAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1632
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 Db 1454 GCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1513
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 Db 1514 GTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1570
 QY 1753 CCGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1812
 Db 1571 CCGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1630
 QY 1813 GCCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1872
 Db 1631 GCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1690
 QY 1873 GCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1932
 Db 1691 GCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1750
 QY 1933 TGACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1949
 Db 1751 GTTATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1767
 RESULT 6
 ABA00331
 ID ABA00331 standard; cDNA, 1879 BP.
 AC ABA00331;
 XX
 DT 09-DEC-2002 (first entry)
 XX
 DE Rat CARD-9 cDNA.
 XX
 KW Gene: rat; human; caspase recruitment domain; CARD-9; CARD-10;
 KW CARD-11; apoptosis; inflammation; cell growth; cell death;
 KW lymphocyte activation; cancer; melanoma; autoimmune disease;
 KW arthritis; neurological disorder; Alzheimer's disease; ss.
 XX
 OS Rattus rattus.
 XX
 FH Key location/Qualifiers
 FT CDS 113..1173
 FT /tag= a
 FT /product= "CARD-9"
 XX
 PN WO200270652-A2.
 PD 12-SEP-2002.
 XX
 PF 28-FEB-2002; 2002WO-US06147.
 XX
 PR 02-MAR-2001; 2001US-0798412.
 XX

PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Bertin C;
 XX
 DR WPI; 2002-698749/75.
 DR P-PSDB; AAC79552.
 XX
 PT CARD-9, CARD-10 or CARD-11 polypeptides and polynucleotides, useful for
 PT treating disorders associated with inappropriate apoptosis or
 PT lymphocyte activation, e.g. cancer
 XX
 PS Disclosure; Fig 1; 151pp; English.
 XX
 CC This sequence encodes rat caspase recruitment domain (CARD)-9,
 CC CARD proteins play roles in apoptotic and inflammatory signalling
 CC pathways. CARD-9, -10 and -11 participate in the network of
 CC interactions that modulate caspase activity. They are thought to be
 CC useful as modulating agents for regulating a variety of cellular
 CC processes including cell growth and cell death. CARD proteins and
 CC nucleic acids are useful for treating a disorder associated with
 CC inappropriate apoptosis or lymphocyte activation or for diagnosing
 CC subjects having or that are at risk of developing a disorder associated
 CC with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such
 CC as cancer e.g. melanoma, autoimmune disorders e.g. arthritis, or
 CC neurological disorders e.g. Alzheimer's disease.
 XX
 SX Sequence 1879 BP; 496 A; 503 C; 578 G; 302 T; 0 other;
 Query Match 48.7%; Score 1060.2; DB 24; Length 1879;
 Best Local Similarity 76.2%; Pred. No. 1.1e-175;
 Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;
 QY 76 GCGGCCAGGCTCCTGATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 135
 Db 46 GTGCCATTAACCCAGGAGGAGATCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 101
 QY 136 CTGCTGAGGCGCATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 195
 Db 102 CTACAGAGGACATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 161
 QY 196 TCGGGGTGAGCTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 255
 Db 162 TCGGGGTGAGCTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 221
 QY 256 GCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 315
 Db 222 GCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 281
 QY 316 GCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 375
 Db 282 GCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 341
 QY 376 TGAGCTTCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 435
 Db 342 TGAGCTTCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 401
 QY 436 AGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 495
 Db 402 AGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 461
 QY 496 AGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 555
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 Db 522 TGAGCTTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 581
 QY 616 ACCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 675
 Db 582 ACCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 641
 QY 676 GCTGCAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 735


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Db      642 GCTGCAAGATGAACTACGACCTGCGCCCTGCGCTCACTGAGTGAAGAAAG 701
Qy      736 GCGCCGCGCTCATGCGGAAACCTGACCTGAGCTGAGATTGACCAAGCTCAAGCAAGCC 795
Db      702 GAGCAGCACTCATGCGGAAACCTGACCTGAGCTTGAAGTGAACCACTCAAGCAAGCC 761
Qy      796 TCATGAAGCGGAGAGCACTGCAAGGTGAGGCGCAAGCAAGCTGAAAGCTGAGGCAAG 855
Db      762 TCATGAAGCGGAGAGCACTGCAAGGTGAGGCGCAAGCAAGCTGAAAGCTGAGGCAAG 821
Qy      856 CCATGAGCAAGCGGCGCAAGCAAGGTGAGGCGCTGAGGAGCTGAGCAAGAGAGCCCTGCG 915
Db      822 CCATGAGCAAGCGGCGCTGAGCAAGGTGAGGCGCTGAGGAGCTGAGCAAGAGAGAGCTTGT 881
Qy      916 TCCAGCGCGCGGCTGAGCAAGGTGAGGCGCTGAGGAGCTGAGGAGAGCTGAGCAAGAGCA 975
Db      882 TGACGCGCGCGGCTGAGCAAGGTGAGGCGCTGAGGAGCTGAGGAGAGCTGAGCAAGAGCA 941
Qy      976 GCGCCCTCATCTCAGATCTGAGAGAGCTGAGGAGAGCTGAGGAGAGCTGAGGAGAGCTGAGGAG 1035
Db      942 GCGCATATCATCTCAGATCTGAGAGAGCTGAGGAGAGCTGAGGAGAGCTGAGGAGAGCTGAGGAG 1001
Qy      1036 AGGCGCAACCATCTTCTCCCTGCGAAGAGCTGCGCAGAGGCGAGAGGCGCGAGCTGCG 1095
Db      1002 AGGCGCAACCATCTTCTCCCTGCGAAGAGCTGCGCAGAGGCGAGAGGCGCGAGCTGCG 1061
Qy      1096 GGTGTCATGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1155
Db      1062 GGTGTCATGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1121
Qy      1156 AGATGTACAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1215
Db      1122 AGATGTACAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1181
Qy      1216 GGAAGCAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1275
Db      1182 GGAAGC----- 1186
Qy      1276 CCTCGGAGCCTCTGCTTGAAGTGGAGCGCGCGGCGAGGCGCCAGAGGCGAGAGCTTGGGG 1335
Db      1187 ----- 1186
Qy      1336 CCTCTCATGAGAGGTGCGCTTGTCTGCTCCGCTGAGGCGCTTACGCGCGGAGAGAGCTG 1395
Db      1187 -----CAGGCTATGACCTTCAAGGAGAGAGCTG 1213
Qy      1396 CAGGCGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1455
Db      1214 CATGCAACAGTGTGCTCAAGAGCTTCAAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAG 1273
Qy      1456 CTGAGGCGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1515
Db      1274 CTGAGTGAAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1333
Qy      1516 GCGCTGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1575
Db      1334 GCGCGTGAAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1393
Qy      1576 GAAATAGCTTCAAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1632
Db      1394 GAAATAGCTTCAAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1453
Qy      1633 ACCAGAGCTTCAAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1692
Db      1454 GCGCAGCTTCAAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1513
Qy      1693 GCTCTGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1752
Db      1514 GTTCTGAAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1570
Qy      1753 CCGCGCGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1812

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Db      1571 CCCCCGAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1630
Qy      1813 GCGCTCAAGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1872
Db      1631 GCGCTCGGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1690
Qy      1873 GCGAGCGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1932
Db      1691 GCGAGCGAGAGAGAGAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1750
Qy      1933 TGACTTGGCTGAGAGC 1949
Db      1751 GTTATTTGAAGAGATG 1767

RESULT 7
AAH08620
ID AAH08620 standard; cDNA; 765 BP.
XX
AC AAH08620;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:5455.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 1; SEQ ID 5455; 2537bp + CD ROM; English.
XX
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH0166 to AAH1628 and

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DB 233 GGAACAGAGAAATCGTGGCCCTGAAAGGCCAGCCGAGCTGGCGGCGCATTTGGGCGCTTT 174
QY 2004 GTTAAGCGGACATCTTTGGCGGAGCCAGTGGCGGTGCTCAACACCCCATGACACAGCC 2063
DB 173 GTTAACCGGACATCTTTGGCGGAGCCAGTGGCGGTGCTCAACACCCCATGACACAGCC 114
QY 2064 ATCTGTGTAATCTCAGAGATCTGTTTCACCATGTAACACACATATGATGAT 2123
DB 113 ATCTGTGTAATCTCAGAGATCTGTTTCACCATGTAACACACATATGATGAT 54
QY 2124 TGTATTAGTGTGTAAGAAACACAGCTGCTGTAATTAACAGACGGGTGACCCGC 2176
DB 53 TGTATTAGTGTGTAAGAAACACAGCTGCTGTAATTAACAGACGGGTGACCCGC 1

RESULT 9
ABX11430
ID ABX11430 standard; cDNA, 3744 BP.
XX
AC ABX11430;
XX
DT 09-MAY-2003 (first entry)
XX
DE Human caspase recruitment domain containing protein, CARD-11X, cDNA.
XX
XX CARD, caspase recruitment domain; apoptosis; cell adhesion; inflammation;
XX cytolysis; receptor signaling; cancer; glioma; carcinoma; adenocarcinoma;
XX CARD-containing polypeptide associated disorder; sarcoma; melanoma; ss;
XX hamartoma; leukemia; lymphoma; keratinocyte hyperplasia; neoplasia;
XX keloid; benign prostatic hyperplasia; inflammatory hyperplasia; fibrosis;
XX restenosis; allergy; arthritis; lupus; Sjogren's syndrome; sepsis; gene;
XX Crohn's disease; ulcerative colitis; graft versus host disease; stroke;
XX abnormal cell death disease; myocardial infarction; heart failure; human;
XX neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV;
XX CARD-11X; caspase activator; caspase inhibitor.
XX
OS Homo sapiens.
XX
FH Key 1..3744 Location/Qualifiers
FT CDS /tag= a
FT /product= "CARD-11X"
FT misc_feature /tag= b
FT /note= "Encodes caspase recruitment domain (CARD)"
FT misc_feature 388..1344 /tag= c
FT /note= "Encodes Ezrin/radixin/moesin (ERM) domain"
FT misc_feature 2175..2514 /tag= d
FT /note= "Encodes post synaptic density disc-large zo-1 (PDZ) domain"
XX
XX US2002164703-A1.
XX
XX 07-NOV-2002.
XX
XX 19-DEC-2001; 2001US-0032159.
XX
XX 21-DEC-2000; 2000US-257457P.
XX
XX (PAWL/) PAWLOWSKI K.
XX (REED/) REED J C.
XX (GODZ/) GODZIK A.
XX
XX Pawlowski K, Reed JC, Godzik A;
XX
XX WPI; 2003-288137/28.
XX P-PSDB; ABG76061.
XX
XX New isolated CARD-containing nucleic acids, useful for the diagnosis
XX and treatment of disorders with aberrant expression or activity of the

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PT CARD-containing polypeptide, such as cancer, stroke, arthritis, heart
PT failure and AIDS
XX
XX Claim 1; Fig 2; 34pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX caspase recruitment domain (CARD) containing polypeptide. CARD containing
XX polypeptides are involved in apoptosis (as caspase activators and caspase
XX inhibitors), cell adhesion, inflammation and cytokine receptor
XX signaling. The methods and compositions of the present invention are
XX useful for the diagnosis and treatment of disorders associated with the
XX aberrant expression or activity of the CARD containing polypeptide such
XX as cancer, glioma, carcinoma, adenocarcinoma, sarcoma, melanoma, keloid,
XX hamartoma, leukemia, lymphoma, keratinocyte hyperplasia, neoplasia,
XX benign prostatic hyperplasia, inflammatory hyperplasia, fibrosis,
XX restenosis, allergies, inflammatory diseases such as arthritis, lupus,
XX Sjogren's syndrome, Crohn's disease, ulcerative colitis, graft versus
XX host disease, sepsis, abnormal cell death diseases such as stroke,
XX myocardial infarction, heart failure, neurodegenerative diseases like
XX Parkinson's disease and Alzheimer's disease, and HIV infection. The
XX present sequence represents cDNA encoding the human caspase recruitment
XX domain containing protein, CARD-11X.
XX
XX Sequence 3744 BP; 950 A; 1076 C; 1117 G; 601 T; 0 other;
XX
XX
XX Query Match 17.3%; Score 375.8; DB 25; Length 3744;
XX Best Local Similarity 56.9%; Pred. No. 1.7e-56;
XX Matches 817; Conservative 0; Mismatches 547; Indels 73; Gaps 4;
XX
XX 157 ACGAGAACGATGACGAGTGTGAAAGCTCTGAGGGCTTCGGGTGACGCTCACTCG 216
XX 26 AGGAGGAAGAGAGACCCCTTGAGAGATGAGAGTGAACCGGACATGCTACCGCGT 85
XX 217 TCATGACCCCTCAGCATCAACCTTACCTGCGGAGTGCAGAGTCTCAACCTGATG 276
XX 86 ATATCAACCTGCGCAAGCTCAAGCCCTACCTGCTGAGTGAAGTATGATGAGCAGG 145
XX
XX 277 ATGAGAGACAGTGTGACGACACCCCAACCTGCTATCCGAAACGAAATGGGTGTGC 336
XX 146 ATGAAGATGAAGTGTGATATGCCCCCTATGCTGCATCCAGATCAACCGACAGCCGCG 205
XX 337 TCCGGAATCCTGAGCGGACCGGACCAAGGGGCTAGCGCTTCCTCGAGAGCTCG 396
XX 206 TGTGGAATCTTACATACCAAGGCGCAAGGGGCTATGAGTCTTCTTGAGAGCTTAG 265
XX
XX 397 AGCTTACTACCCGAGCTGTACAGAGGTCAAGAGGTCAAGGACGAGCCGCGCTCTCT 456
XX 266 AATTTATTACCAAGATCTGTACAACTGAGTGAAGGAAAGAGCCACTCGAGATCT 325
XX 457 CCATATCATGACGCGTCCGGGAGTCAAGGCTGACTCACTGCTGATGACTGAGTCA 516
XX 326 CCACATGTGTGTGAGAGAGGACCAAGGCGCTCACCACTCTGATGAGAGGCTCA 385
XX
XX 517 TGAAGCTGGAAGAAGAGTGCAG-----GACGTACCGGCGCTCG 555
XX
XX 386 TCAAGCTGCAAGAGATGAAGGCCAAGACCTGCAACGCTGCAAGTGTGCGAGGT 445
XX 556 TGAGCTCCAAAGATGATCTCATCAAGAGCTGCGGGTGAAGGACAGCTGCTCGCAAGC 615
XX 446 TCGGCACTGAGAGATGAAGAAAGCAGATGACGCTGACGCGCTGAGAGCTGCTAACCT 505
XX
XX 616 ACCAGAGCGTGTGCAAGAGCTCAAGAGAGAGTGTGAGAGCCGCGACCGGAGCTCAAGC 675
XX 506 TCCAGAGAGCGTACTACAAAGATGAAGAGAGCGGAGACAGTACATGACGAGTGTCA 565
XX
XX 676 GCTGCAAGAGAGAACTACGACTGCGCATTCGCTGCGGACCAAGAGTGAAGAGAGG 735
XX 566 AGGTGAAGAGCACTACCACTTAGCCATGCGCTAGCCACAGTCAAGTGAAGAGAA 625
XX
XX 736 GCGCGCGCTCATGCGGAACGCTGACCTGAGAGTGAAGTGAAGAGCTCAAGCAGCC 795
XX 626 ACATGCGGCTCATGAGAGCCGAGACCTCAACTGAGATGATGATGATGATGATGATG 685

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QY 796 TCATGAAGGCCGAGAGCACTGCGAGGTGAGCGCAAGCAGCTGGAAGCTCAGGCGACG 855
DB 686 TGATATAGATGAGAGAGATGTAAAGCTGAGAGAAATAGTCTTAAACTGAAGATG 745
QY 856 CCATGAGAGACGGGCCCAAGCAGAGAGTGTCTGTGGAGCTGCGACAGAGAGAGCCCTGC 915
DB 746 ACATTGAAATCGGCCCAAGAGAGAGAGGTTCTTGAATCGAGCGGAGAAATGAATGC 805
QY 916 TCACAGGCCCGGGGTGACAGAGCTGAGAGGCTCCGTCAGAGAGGAAA-----GCTGA 966
DB 806 TGAAGACAAAACACAGAGAGCTGCAATCTCATTCAGAGCGCGAGAGCCGAGCTGCGAG 865
QY 967 ACAGAGACAGCCCTTACATCAGAGTACTGAGAGAGAGATGCTGCGAGAGAGCTGCGAGCC 1026
DB 866 ACTGACAGACAGCCATCTTGAACATCTTGAACACAGACCCGAGAGAGCCCTGAGAGACA 925
QY 1027 ACCAGAGACAGGCCACCACTTCTCCCTGCGCAAGAGACCTTCCGACAGGCGAGGCC 1086
DB 926 GGCAGAGAGCTGTGACAGAGATCTACAACCTGCAAGAGAGAGGCCCGCAGAGAGAGC 985
QY 1087 GAGCCCTCCGCTGATGAGAGAGAGAGATCTTCAAGCTGCAAGTGTCTGCACTACGTA 1146
DB 986 TGCAGAGCAAGTACCTGAGAGAGAGAGAGAGAGCTGAGAGTCAAGTCTCAACCTGGAA 1045
QY 1147 AGGACTCCAGATGTATACAGAGACCGGACATCGAGGCTGCTGAGAGAGAGAGCTG 1206
DB 1046 AGGACTGTAAATGTATACAGAGACCGGACATGACAGTGTATGCTGCAAGTGTAGAGAG 1105
QY 1207 CCATTGAGCGGAGCCAGAGACACAAATGAGAGGCTGTGACAGCTCCGCGCCAGCG 1266
DB 1106 AGCGGAGCGGAGCCAGAG-----ACA 1127
QY 1267 GCTTGAAGTCTCCGAGAGCTCTGTGAGATTGAGGCGCGCGGCGAGAGGCCAGAGGCA 1326
DB 1128 GCGTGTGCTTTCAGAGAGACCTGATCACTA-----AGCTCAACAGAGAGCTGCACT 1182
QY 1327 AGCTTGGGGCCCTTCACTGAGGAGTGGCGCTGTGCTGTCCGCTCAGGCGCATAGCCAGCG 1386
DB 1183 AGCAAGGGTGGAGCCATCGCTGTGATCGCTTAAATGAAGAGGCTTTCAGCTCCGGA 1242
QY 1387 GAGAGAGCTGACAGACAGACAGCCCGGGGCTGACAGAGAGAGAGCGGCTCGGAAGCAG 1446
DB 1243 GATGAAGCTGAGACAGACTACTTCCAGTCTTAATCGAAAGAGACAGATACAGGAGCAG 1302
QY 1447 GTGCGGAGCTGGGGGAGAGAGCGGATAGAGCTGACAGCTGACAGGTTTCAAGTGAAGCG 1506
DB 1303 ATCCGAGAGCTGAGAGAGAGAGAGAGAGAGATGAGATGAGATGCTGCGCGGAGAGCC 1362
QY 1507 CAGTACTGCGCTGAGAGAGAGGCTCAGGCGGAGAGAGAGAGAGAGAGCTGCTGCTG 1563
DB 1363 TGCATCGTCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1419

RESULT 10
AAS05389
ID AAS05389 standard; cDNA; 4275 BP.
AC AAS05389;
DT 12-SEP-2001 (first entry)
DE Human caspase recruitment domain, CARD-11 cDNA sequence.
XX Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
XX apoptosis; hyperproliferative disorder; autoimmune; neurological;
XX inflammatory disorder; viral infection; stress-related response; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 327..3770
XX FT /tag= a
XX FT /product= "CARD-11"

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PT /note= "ORF is specifically claimed"
XX
XX WO200140468-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 01-DEC-2000; 2000WO-US32716.
PF
XX
XX 03-DEC-1999; 99US-0168780.
PR 18-FEB-2000; 2000US-0507533.
PR 25-FEB-2000; 2000US-0513904.
PR 10-OCT-2000; 2000US-0685791.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Bertin J.
PI
XX WPI; 2001-367809/38.
DR
XX P-PSDB; AAU01207.
DR
XX
XX Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10,
PT CARD-11, useful as targets for therapy, as immunogens, and in screening
PT and detection assays -
XX
XX Claim 2; Fig 14A-14C; 145pp; English.
PS
XX
XX The present sequence encoding for novel human caspase recruitment
XX domain, CARD-11 is isolated from a human T-cell cDNA library.
XX Also described are novel human sequences for CARD-9 and CARD-10
XX (AAU01205, AAU01206) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and
XX CARD-11 interact with Bcl-10 which is thought to activate nuclear factor
XX (NF)-kappaB and apoptosis. The sequences of the invention can be used for
XX treating a disorder associated with abnormal levels of apoptosis by
XX modulating the expression or activity of CARD-9, CARD-10, or CARD-11.
XX They can be used for the treatment of hyperproliferative disorders
XX (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus),
XX neurological disorders (e.g. Alzheimer's disease), inflammatory disorders
XX (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD
XX polypeptide, polynucleotide and an antibody which selectively binds to
XX CARD can be used in screening and detection assays (e.g. chromosomal
XX mapping, tissue typing), predictive medicine (prognostic assays,
XX monitoring clinical trials, and therapy (treatment and prophylaxis). The
XX CARD polypeptide may be used to screen for drugs that bind to and/or
XX modulate it. CARD sequences are potential targets for regulating
XX inflammation, cancer, NF-kappaB signaling, stress-related response and
XX apoptosis in human disease. A host cell containing a polynucleotide
XX encoding CARD can be used to create transgenic animals.
XX
XX Sequence 4275 BP; 1045 A; 1255 C; 1320 G; 655 T; 0 other;
SQ
XX
XX Query Match 17.1%; Score 372.2; DB 22; Length 4275;
XX Best Local Similarity 60.5%; Pred. No. 7.2e-56;
XX Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;
XX
XX 157 ACAGAGACGATGACGAGTGTGAGACGTCCTGAGAGGCTTCCGGTGAAGCTCACTCG 216
DB 352 AGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
QY 217 TCATGACCCCTCAGAGATACACCTTACCTGGGAGAGAGAGAGAGAGAGAGAGAGAG 276
DB 412 ATATCAACCTTGCAGAGCTCAGCCCTTACCTGCTGAGAGAGAGAGAGAGAGAGAGAG 471
QY 277 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
DB 472 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
QY 337 TCCTGACATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
DB 532 TGTGAGATTTATACATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 591
QY 397 AGCTTACTACTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 456
DB 592 AATTATTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 651

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QY 457 CCATGATCATCGACGGCTCCGGGAGTCAAGCCTGACCTGCTGATGACTGAGTCA 516
DB 652 CCACCATTTGGTGGAGGAAAGCCACGAGGGCTTCACGACTTCTGATGAACGAGTCA 711
QY 517 TGAAGCTGCAAGAAAGGTGACAGGAC-----CTGACCGGCGCTGC 555
DB 712 TCAAGCTGACGACCGCATGAAAGGCCAAGGACCTGCAACGCTGCGAGCTGCGCCAGGT 771
QY 556 TGAGCTCCAAAGATGACTTCATCAGAGAGTGGCGGTGAGAGACAGCTCTGCGCAAC 615
DB 772 TGGGGACGCTGAGAGATGAGAGAGAGATGACGCTGACGCGCTGGAGCTCTAACT 831
QY 616 ACCAGAGCGTGTGACAGAGCTCAAGAGAGAGTGCAGAGCGCGCAGCGGAGCTCAAC 675
DB 832 TCCAGAGCGGCTACTACAGATGAAAGGAGAGCGGAGCAGCTCAATGACGAGCTGTCA 891
QY 676 GCTGCAAGAGAGAACTACGACCTGGCCCTGGCGCGCACAGAGTGAAGAGAGAG 735
DB 892 AGGTGAAGAGACGACMACTACACTAGCCATGCGCTACGACAGCTCAGTGAAGAGAGA 951
QY 736 GCGCGCGCTCATGCGGACCGTGAACCTGACGCTGAGATTGACAGCTCAAGCAGACGC 795
DB 952 ACATGCGCTCATGAGAGAGCGGAGACTTCAACTCGAGTGCATGACTTAAGCAGCGGT 1011
QY 796 TCAATGAAGCGGAGACGACTGAGAGTGAAGCGCAAGCAGCAGCTGAAGCTCAGGACG 855
DB 1012 TGATATAGATGAGAGAGAGATGTAAGTGAAGAAATCACTCTTAAACTGAAGATG 1071
QY 856 CCATGAGACGCGGCCCAAGCAGAGCTGCTGGAGAGTGCACGACAGAGAGAGCCCTGC 915
DB 1072 ACATGAAATTCGGCCCAAGAGAGAGAGGTTCTGGAATCTGAGACGCGGAGAAATGAAATG 1131
QY 916 TCCAGCGCGGCTGACAGAGCTGAGAGCTCCGCTCCAGAGAGGAGAA-----GCTCG 966
DB 1132 TGAAGACAAACAAACAGAGCTGACGTCATCAATCCAGCGCGGAGAGCGCAGCTGCGAG 1191
QY 967 ACAGAGACAGCGCCCTATCATCAGGTACTGAGAGAGAGAGTGGCGGACAGGCTCCGAGAC 1026
DB 1192 ACTGAGCAAGGCGCATCTTGACATCTTGGAACACGACCGCAGAGAGCGCTTGAAGACA 1251
QY 1027 ACCAGAGACAGGCGCACACCATCTTCTCCCTGGCAAGAGACTCCCGCAGAGGCGCC 1086
DB 1252 GCGACGAGCTGTGTAACAGATCTACAACTGACAGAGAGAGCGCCGCAAGCAGAGAG 1311
QY 1087 GAGCGCTCCGCTGATGAGAGAGAGAGATGTTCCAGCTGCAAGTGGCTTGGCACTACGTA 1146
DB 1312 TGCAGACCAAGTACCTGAGAGAGAGAGAGAGAGAGCTGAGCTCAAGTCTCAACCTGGGAA 1371
QY 1147 AGGACTCCAGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
DB 1372 AGGACTGTAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
QY 1207 CCATTGAGCGGAGCCAG 1223
DB 1432 AGCGGAGCGGAGCCAG 1448

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RESULT 11
 ABA00334
 ID ABA00334 standard; cDNA; 4276 BP.

AC ABA00334;
 AT 09-DEC-2002 (first entry)
 DE Human CARD-11 cDNA.
 XX Gene; rat; human; caspase recruitment domain; CARD-9; CARD-10;
 KW CARD-11; apoptosis; inflammation; cell growth; cell death;
 KW lymphocyte activation; cancer; melanoma; autoimmune disease;
 KW arthritis; neurological disorder; Alzheimer's disease; ss.
 XX

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OS Homo sapiens.
XX Key Location/Qualifiers
PH 328..3771
PT CDS /*tag= a
FT /product= "CARD-11"
XX
XX MO200270652-A2.
XX
XX 12-SEP-2002.
XX
XX 28-FEB-2002; 2002WO-US06147.
XX
XX 02-MAR-2001; 2001US-0738412.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Bertin J;
XX
XX WPI; 2002-698749/75.
XX
XX P-PSDB; AAG79555.
XX
XX CARD-9, CARD-10 or CARD-11 polypeptides and polynucleotides, useful for
XX treating disorders associated with inappropriate apoptosis or
XX lymphocyte activation, e.g. cancer
XX
XX Disclosure; Fig 14; 151pp; English.
XX
XX This sequence encodes human caspase recruitment domain (CARD)-11.
XX CARD proteins play roles in apoptotic and inflammatory signaling
XX pathways. CARD-9, -10 and -11 participate in the network of
XX interactions that modulate caspase activity. They are thought to be
XX useful as modulating agents for regulating a variety of cellular
XX processes including cell growth and cell death. CARD proteins and
XX nucleic acids are useful for treating a disorder associated with
XX inappropriate apoptosis or lymphocyte activation or for diagnosing
XX subjects having or that are at risk of developing a disorder associated
XX with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such
XX as cancer e.g. melanoma, autoimmune disorders e.g. arthritis, or
XX neurological disorders e.g. Alzheimer's disease.
XX
XX Sequence 4276 BP; 1045 A; 1256 C; 1320 G; 655 T; 0 other;
XX
XX Query Match 17.1%; Score 372.2; DB 24; Length 4276;
XX Best Local Similarity 60.5%; Pred. No. 7.2e-56;
XX Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;
XX
QY 157 ACAGAGACGATGACGAGTGTGAAAGTCTGAGAGGCTTCGGGTGACGCTCACTCGG 216
DB 353 AGGATGAAGAGAGACGCTGTGGAGAAATGTGAGTGTACCGGACATGCTCACCGCT 412
QY 217 TCATGACCCCTCAGAGATCAACCTTACCTGGGAGTGAAGTCCGAACTGTATG 276
DB 413 ATATCAACCTTCCAGAGCTCAGGCTCAGGCTTACCTGCTGAGTGAAGTCAATGAGCAG 472
QY 277 ATGAGAGAGAGTGTGACGAGACCCCAACCTGTATCCGCAAGAGAGAGTGTGTC 336
DB 473 ATGAGATGAATGCTTATATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATG 532
QY 337 TCTGTGACATCTGTGACGCGGAGCCGCAAGAGGCTTACGCTTCTCGAGAGCTTGC 396
DB 533 TGTGTGACATTTTACATACCAAGGAGCAAGGAGGCTATGTGTCTTGTGAGAGCTTGA 592
QY 397 AGCTTACTACCCGAGCTGTTCAGAGAGTCAAGAGTCAAGAGAGAGAGAGAGAGAGAG 456
DB 593 AATTATATTAACCAAGAGTGTACAACTGTGTACTGTGGAAGAGAGAGAGAGAGAGAG 652
QY 457 CCATGATCATGACGCGTCCGGGAGTCAAGGCTGACCTGAGCTGATGATGAGTCA 516
DB 653 CCACCATTTGGTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCA 712
QY 517 TGAAGCTGCAAGAAAGGTGACAGGAC-----CTGACCGGCGCTGC 555

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Db 713 TCAAGCTGACGACGATGAGAGCCAGACCTGCAAGCTGCGAGCTGCGCCAGGT 772
 QY 556 TGAGCTCCAAAGATGATCTTCATCAAGAGAGCTGCGGATGAGAGCAAGCTGCTGCGGACG 615
 Db 773 TGGGCGAGCTGCGAGATGAGAGAGAGAGATGACGTGACGCGCTGAGAGCTGCTAACT 832
 QY 616 ACCAGAGCGCTGTGACAGAGCTCAAGAGAGAGTGCAGAGCGCGAGCCGAGCTCAAGC 675
 Db 833 TCCAGAGCGCTGCTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 892
 QY 676 GCTGCAAG 735
 Db 893 AGGTGAG 952
 QY 736 GCGCGCGCTCATGCGGAGCGGTGACCTGAGCTGAGAGATGACAGCTCAAGCAGAGCC 795
 Db 953 ACATGCGCTCATGAG 1012
 QY 796 TCATGAGAGCGCGAG 855
 Db 1013 TGAATTAAGATGAG 1072
 QY 856 CCATGAG 915
 Db 1073 ACATGAG 1132
 QY 916 TCCAGAGCGCGGATGAG 966
 Db 1133 TGAAGACCAAAACAG 1192
 QY 967 ACAG 1026
 Db 1193 ACATGAG 1252
 QY 1027 ACCAG 1086
 Db 1253 GCGAG 1312
 QY 1087 GACGCGCTCCGATGAG 1146
 Db 1313 TCGAG 1372
 QY 1147 AGGATCTCAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
 Db 1373 AGGATCTGTAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
 QY 1207 CCATGAGCGGAG 1223
 Db 1433 AGCGGAG 1449

RESULT 12
 ACCS0413
 ID ACCS0413 standard; cDNA; 1663 BP.
 XX
 AC ACCS0413;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human secreted protein coding sequence, SEQ ID 80.
 XX
 KM Cardiac; antiarrhythmic; antiarteriosclerotic; vasotrophic; cytostatic;
 KM vulnerable; antiinflammatory; neurotrophic; neuroprotective;
 KM antiparkinsonian; gene therapy; human; cardiovascular disorder;
 KM gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200295010-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 19-MAR-2002; 2002WO-US09785.

XX 21-MAR-2001; 2001US-277340P.
 PR 19-JUL-2001; 2001US-306171P.
 PR 13-NOV-2001; 2001US-331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCL INC.
 PI Rosen CA, Ruben SM;
 DR WPI; 2003-129429/12.
 PT Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating
 PT cardiovascular disorders such as arrhythmia -
 PS Claim 21; SEQ ID 80; 1681bp; English.
 XX
 CC The present invention relates to novel human secreted proteins
 CC (ABR47533-ABR48145) and their coding sequences (ACCS0344-ACCS0856). The
 CC proteins and their coding sequences are useful for the preparation of a
 CC diagnostic or pharmaceutical composition for diagnosing or treating a
 CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
 CC coronary arteriosclerosis and myocardial ischemia), neural disorders,
 CC immune system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of hematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism.
 CC Note: The sequence data for this patent was published in electronic
 CC format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 1663 BP; 414 A; 481 C; 512 G; 256 T; 0 other;
 Query Match 16.9%; Score 367.4; DB 25; Length 1663;
 Best Local Similarity 82.4%; Pred. No. 4.6e-55;
 Matches 467; Conservative 0; Mismatches 26; Indels 74; Gaps 1;
 QY 1684 CCCTTTGACGCTCTGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1743
 Db 966 CCTCAG 1025
 QY 1744 AGCGGAG 1803
 Db 1026 AGCGGAG 1085
 QY 1804 AGGAG 1863
 Db 1086 AGGAG 1145
 QY 1864 AACACACAG 1910
 Db 1146 AACACACAG 1205
 QY 1911 ----- 1910
 Db 1206 CGACCAAGGAG 1265
 QY 1911 -GGAG 1969
 Db 1266 CGAG 1325
 QY 1970 GCGCCAG 2029

DB 1326 GGGCCGACCGGAGCTGCGGCGCATTTGGGGCCGTTTGAAGCCGCACTCATTTTGGCGAGG 1385
 QY 2030 CCATGGGGGTGTCACACCCCATGACAGCGGCATCTGTAACTCGATCTGTTCT 2089
 DB 1386 CCATGGGGGTGTCACACCCCATGACAGCGGCATCTGTAACTCGATCTGTTCT 1445
 QY 2090 GTTTCACCATGTAAACACAAATACATGATGATTTGTTAGAAAACAGAGCTG 2149
 DB 1446 GTTTCACCATGTAAACACAAATACATGATGATTTGTTAGAAAACAGAGCTG 1505
 QY 2150 CGTAATATAACAGACGCGGTGACCCGC 2176
 DB 1506 CGTAATATAACAGACGCGGTGACCCGC 1532

RESULT 13
 ABZ71230
 ID ABZ71230 standard; cDNA, 1663 BP.
 XX
 AC ABZ71230;
 DT 03-APR-2003 (first entry)
 XX
 DE Human secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:51.
 XX
 KM Human; secreted protein; digestive disorder; gastrointestinal disorder;
 KM mouth; oesophagus; stomach; small intestine; large intestine; liver;
 KM biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
 KM immune disorder; inflammation; infection; wound healing; drug screening;
 KM chromosome identification; chromosome mapping; cytostatic;
 KM anti-inflammatory; immunosuppressive; vulnerrary; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200276488-A1.
 PD 03-OCT-2002.
 XX
 PF 19-MAR-2002; 2002MO-US08276.
 XX
 PR 21-MAR-2001; 2001US-277340P.
 PR 19-JUL-2001; 2001US-306171P.
 PR 13-NOV-2001; 2001US-331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI, 2003-029900/02.
 DR P-PSDB; ABR00051.
 XX
 PT New human secreted proteins and nucleic acids, useful for detecting,
 PT preventing, diagnosing, prognosticating, treating and/or ameliorating
 PT e.g. gastrointestinal diseases and disorders, or cancers -
 XX
 PS Claim 21; Page 782; 1216P; English.
 XX

CC of the invention may be used for chromosome identification, chromosome
 CC mapping, in gene therapy, for identifying individuals from minute
 CC biological samples, as hybridisation probes, and as molecular weight
 CC markers. The present sequence represents a human secreted protein-
 CC encoding cDNA clone of the invention.
 XX
 SQ Sequence 1663 BP; 414 A; 481 C; 512 G; 256 T; 0 other;
 Query Match 16.9%; Score 367.4; DB 25; Length 1663;
 Best Local Similarity 82.4%; Pred. No. 4,6e-55;
 Matches 467; Conservative 0; Mismatches 26; Indels 74; Gaps 1;
 QY 1684 CCCTTTCAGCTCTGACCAAGAGCAGTTTGGGGAACCCCATGACGAGCTTACG 1743
 DB 966 CCTCAGGGGAGCGCGCGGAGCCGAGCCTTCCCTTCCAGGACGAGGCTGAGC 1025
 QY 1744 AGCGGGAGCGCGCGCGGAGAGAGAGCGCGCGCTTCAAAGAGTTTGAAGTACCGC 1803
 DB 1026 AGCGGGAGCGCGCGGAGAGAGAGCGCGCGCTTCAAAGAGTTTGAAGTACCGC 1085
 QY 1804 AGAAGCGCGCGCTCAGAGAAAGATGACAGAAAGATGCGCGAGGAGAGAGAGAGAG 1863
 DB 1086 AGAAGCGCGCTCAGAGAAAGATGACAGAAAGATGCGCGAGGAGAGAGAGAGAG 1145
 QY 1864 AACACACGCGGACGACCAACACCGACATGAGGCGCTCTAGCCGCA----- 1910
 DB 1146 AACACACGCGGACGACCAACACCGACATGAGGCGCTCTAGCCGCAAGCGAGGCC 1205
 QY 1911 ----- 1910
 DB 1206 CGACCAAGGACACCAACCGCGCGCGCTCTCTGACCCCGGAGGCGCGAGCGCTG33G 1265
 QY 1911 -GCAACTTCCCCGAGCGCTGCTGACTTGGCTTGAAGAGAACTGTGTCCTGAA 1965
 DB 1266 CGCAACTTCCCCGAGCGCTGCTGACTTGGCTTGAAGAGAACTGTGTCCTGAA 1325
 QY 1970 GGGCCAGCGGAGCTGCGGCGGATGGGGCGCTTGTAAAGCGGACATCATTTTGGAGG 2029
 DB 1326 GGGCCAGCGGAGCTGCGGCGGATGGGGCGCTTGTAAAGCGGACATCATTTTGGAGG 1385
 QY 2030 CCATGCGGGTGTCTACACACCCCATGACAGCGCATCTGTAACTTCAAGATCTGTTCT 2089
 DB 1386 CCATGCGGGTGTCTACACACCCCATGACAGCGCATCTGTAACTTCAAGATCTGTTCT 1445
 QY 2090 GTTTCACCATGTAAACACAAATACATGATGATTTGTTAGAAAACAGAGCTG 2149
 DB 1446 GTTTCACCATGTAAACACAAATACATGATGATTTGTTAGAAAACAGAGCTG 1505
 QY 2150 CGTAATATAACAGACGCGGTGACCCGC 2176
 DB 1506 CGTAATATAACAGACGCGGTGACCCGC 1532

RESULT 14
 AAD05585
 ID AAD05585 standard; cDNA, 1687 BP.
 XX
 AC AAD05585;
 DT 17-JUL-2001 (first entry)
 XX
 DE Human secreted protein-encoding gene 7 cDNA clone HDP5H53, SEQ ID NO:17.
 XX
 KM Human; secreted protein; proliferative disorder; cancer; tumour;
 KM foetal abnormality; developmental abnormality; haematopoietic disorder;
 KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KM inflammation; allergy; neurological disorder; Alzheimer's disease;
 KM Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KM skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KM cardiovascular disorder; angogenic disorder; kidney disorder;
 KM gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 KM endocrine disorder; infection; wound healing; vulnerrary;
 KM cell culture; chemotaxis; food additive;

XX	binding partner identification; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	153..536
XX		/*tag= a
XX	sig_peptide	/product= "Human secreted protein"
XX		153..209
XX		/*tag= b
XX	mat_peptide	210..533
XX		/*tag= c
XX		/product= "Human mature secreted protein"
XX	WO200134627-A1.	
XX	17-MAY-2001.	
XX	08-NOV-2000; 2000MO-US30628.	
XX	12-NOV-1999; 99US-0164744.	
XX	30-JUN-2000; 2000US-0215140.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Ruben SM, Komatsoulis GA, Baker KP, Young PE,	
XX	WPI; 2001-316491/33.	
XX	P-PSDB; AAE01776.	
XX	New nucleic acid molecules encoding human secreted proteins, used in	
XX	preventing, treating or ameliorating a disorder, e.g. Alzheimer's and	
XX	Parkinson's diseases and cancers -	
XX	Claim 1; Page 422-423; 567pp; English.	
XX	AA005579-AA005658 represent cDNAs corresponding to 28 human secreted	
XX	protein genes and AAE01770-AAE01849 represent the proteins they encode.	
XX	AAE01850-AAE01860 represent human secreted protein fragments or variants.	
XX	The genes and their secreted proteins are useful for preventing,	
XX	treating or ameliorating medical conditions, e.g., by protein or gene	
XX	therapy. Pathological conditions can be diagnosed by determining the	
XX	amount of the new protein in a sample or by determining the presence of	
XX	mutations in the new genes. Specific uses are described for each of the	
XX	28 genes, based on the tissues in which they are most highly expressed,	
XX	and include developing products for the diagnosis or treatment of	
XX	proliferative disorders, cancer, tumors, fetal and developmental	
XX	abnormalities, hematopoietic disorders, diseases of the immune system,	
XX	AIDS, autoimmune diseases (e.g., Rheumatoid arthritis), inflammation,	
XX	allergies, neurological disorders (e.g., Alzheimer's disease,	
XX	Parkinson's disease), cognitive disorders, schizophrenia, asthma,	
XX	skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,	
XX	cardiovascular disorders, angioelectric disorders, kidney disorders,	
XX	gastrointestinal disorders, pregnancy-related disorders, endocrine	
XX	disorders, and infectious. The proteins can also be used to aid wound	
XX	healing and epithelial cell proliferation, to prevent skin aging due to	
XX	sunburn, to maintain organs before transplantation, for supporting cell	
XX	culture of primary tissues, to regenerate tissues, to identify their	
XX	cognate ligands or binding partners, and in chemotaxis, and can be used	
XX	as a food additive or preservative to modify storage properties.	
XX	Antibodies specific for a protein of the invention can be used in	
XX	alleviating symptoms associated with the disorders mentioned above, and	
XX	in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked	
XX	immunosorbent assay (ELISA). The present sequence represents a human	
XX	secreted protein-encoding cDNA of the invention.	
XX	Sequence 1687 BP; 432 A; 480 C; 514 G; 256 T; 5 other;	
XX	Query Match 16.3%; Score 355.4; DB 22; Length 1687;	
XX	Best Local Similarity 82.1%; Pred. No. 5.6e-53;	
XX	Matches 467; Conservative 0; Mismatches 26; Indels 76; Gaps 2	

1684 CCGTTTGAGCTTCGACACAGAGCGTTTTCGGAAACCCCATGACGACGCGCTGAGC 1743

Db	965	CCCTCAGAGGAGCGCGCCGAGGCCGAGCCTTCCCTTCTCCAGAGCGAGGCTTAGC	1024
Qy	1744	AGCGGGAGCGCCCGAGAAAGAGCGGCGCGCTCTAAAGAGATTTTGAACCTACGC	1803
Db	1295	AGCGGGAGCGCCCGAGAAAGAGCGGCGCGCTCTAAAGAGATTTTGAACCTACGC	1084
Qy	1804	AGGAAGCGCGCTCTCAGGAAGATGCAAGAAAGATGCGCGAGGG- GGAAGAGACCGGGA	1862
Db	1085	AGGAAGCGCGCTCTCAGGAAGATGCAAGAAAGATGCGCGAGGGTGAAGAGACCGGGA	1144
Qy	1863	GAAACACGAGGAGCGAGCAACAACGACACTGAAGGCTCCCTAGCGCGA-----	1910
Db	1145	GAAACACGAGGAGCGAGCAACAACGACACTGAAGGCTCCCTAGCGAGCGC	1204
Qy	1911	-----	1910
Db	1205	CCGACACGAGGAGCAACCAACCGCGCGCTCTGCGACACCGGGGATGCCAGCGCCTAG	1264
Qy	1911	--GAGACTTCCCCGAGCGCTGCTGACTTTGGCTTGAAGAGAAATCTGTCCTGA	1967
Db	1265	GCGCCAGACTTCCCCGAGCGCTGCTGACTTTGGCTTGAAGAGAAATCTGTCCTGA	1324
Qy	1968	AAGGCCACGCGGACCTGCGCGGCGCTTGGGCGCTTGTAAAGCGGCACTCATTTTGGGGA	2027
Db	1325	AAGGCCACGCGGACCTGCGCGGCGCTTGGGCGCTTGTAAAGCGGCACTCATTTTGGGGA	1384
Qy	2028	GGCCATGCGGGTGTCTACACACCCCATGACACCGCATCTGTGTAACTTCAGATCTGT	2087
Db	1385	GGCCATGCGGGTGTCTACACACCCCATGACACCGCATCTGTGTAACTTCAGATCTGT	1444
Qy	2088	CTGTTTCACCATGTAAACAACATATCATGATGATGATTAGTGTAGAAAAACAGC	2147
Db	1445	CTGTTTCACCATGTAAACAACATATCATGATGATGATTAGTGTAGAAAAACAGC	1504
Qy	2148	TGCGTAATTAACAGCACGGGTACCCGC	2176
Db	1505	TGCGTAATTAACAGCACGGGTACCCGC	1533
RESULT 15			
ACCS0719			
ID	ACCS0719	standard; cDNA; 1687 BP.	
XX	ACCS0719;		
DT	12-JUN-2003	(first entry)	
DE	Human secreted protein coding sequence, SEQ ID 386.		
XX			
KX	Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;		
KM	vulnerary; antiinflammatory; nootropic; neuroprotective;		
KM	antiparkinsonian; gene therapy; human; cardiovascular disorder;		
XX	gene; ss.		
OS	Homo sapiens.		
XX			
PN	WO200295010-A2.		
PD	28-NOV-2002.		
PF	19-MAR-2002; 2002WO-US09785.		
PR	21-MAR-2001; 2001US-277340P.		
PR	19-JUL-2001; 2001US-306171P.		
PR	13-NOV-2001; 2001US-331287P.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Ruben SM;		
XX			
DR	WPI; 2003-129429/12.		
XX			

PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating
PT cardiovascular disorders such as arrhythmia -

PS Claim 21; SEQ ID 386; 1881bp; English.

XX
CC The present invention relates to novel human secreted proteins
CC (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The
CC proteins and their coding sequences are useful for the preparation of a
CC diagnostic or pharmaceutical composition for diagnosing or treating a
CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
CC coronary arteriosclerosis and myocardial ischaemia), neural disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism.
CC Note: The sequence data for this patent was published in electronic
CC format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 1687 BP; 432 A; 480 C; 514 G; 256 T; 5 other;

Query Match 16.3%; Score 355.4; DB 25; Length 1687;

Best Local Similarity 82.1%; Pred. No. 5.6e-53; Matches 467; Conservative 0; Mismatches 26; Indels 76; Gaps 2;

QY 1684 CCCTTTGCACTCTGCACCGAGCAAGTCTTTCGGAAACCCCATGACGAGGCTGTAGC 1743
DB 965 CCTTCAGGGAGAGCGGCGGAGGCCGAGCCTTCCCTTCTCCAGAGCGAGGCTGTAGC 1024
QY 1744 AGCGGGGAGCGCCCGAGAGAGCGGCGGCGCTCAAGAGATTTTGAAGAACTACCGC 1803
DB 1025 AGCGGGGAGCGCCCGAGAGAGCGGCGGCGCTCAAGAGATTTTGAAGAACTACCGC 1084
QY 1804 AGGAAGCGCGCCCTCAGGAAGATGCAAGAAAGATGCGCGAGGG-GAAGAGGACCGGGA 1862
DB 1085 AGGAAGCGCGCCCTCAGGAAGATGCAAGAAAGATGCGCGAGGAGGAGGACCGGGA 1144
QY 1863 GAACACCGAGGAGGAGCAACACCGACACTGAGGGCTCTAGCCGCA----- 1910
DB 1145 GAACACCGAGGAGGAGCAACACCGACACTGAGGGCTCTAGCCGAGCGCGAGGC 1204
QY 1911 ----- 1910
DB 1205 CCGGACGAGGAGCAACCCACCGGCGGCGCTCTGCGAACCGGAGGAGCGAGCCCTGG 1264
QY 1911 ---GCAGACTTCCCGAGCGCGTGTGCTGACTTGGCTGGAACGAGAACTGTGGCTCTGA 1967
DB 1265 GCGGCAAGACTTCCCGAGCGCGTGTGCTGACTTGGCTGGAACGAGAACTGTGGCTCTGA 1324
QY 1968 AAGGCCGAGCGGAGCTGCGGAGGCAATTGGGGCCGTTTGTAAAGGCGCACTATTGGGGA 2027
DB 1325 AAGGCCGAGCGGAGCTGCGGAGGCAATTGGGGCCGTTTGTAAAGGCGCACTATTGGGGA 1384
QY 2028 GGCATGCGGAGTGTCAACACACCCCATGACACGCGCATGTGTAACTTCAAGATCTGTT 2087
DB 1385 GGCATGCGGAGTGTCAACACACCCCATGACACGCGCATGTGTAACTTCAAGATCTGTT 1444
QY 2088 CTGTTTCAACATGTAAACACAATATATGATGATTTAGTGTGTAAGAAACACAGC 2147
DB 1445 CTGTTTCAACATGTAAACACAATATATGATGATTTAGTGTGTAAGAAACACAGC 1504

QY 2148 TCGTAATAAACAAGACAGCGGCTGACCCGC 2176
DB 1505 TCGTAATAAACAAGACAGCGGCTGACCCGC 1533

Search completed: February 23, 2004, 10:02:25
Job time : 632 secs

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OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:41 ; Search time 4582 seconds

(without alignments)
11542.239 Million cell updates/sec

Title: US-10-032-159a-19

Perfect score: 2176
Sequence: 1 atccaccaggaagtgacacag.....aaacagcaggggtgacccgc 2176

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_hiv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_pbg.*
27: em_gss_vtl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	933.2	42.9	1104	BX358485 BX358485
2	883.6	94.0	13	BX329048 BX329048
3	800.8	36.8	815	B1524042 B1524042
4	752.8	34.6	775	B1907340 B1907340

5	725.4	33.3	765	9	AU142752
6	699	32.1	722	12	B1905841
7	668	30.7	755	13	B1912159
8	650.4	29.9	1091	13	BX358484
9	645.6	29.7	738	10	B1909365
10	636.2	29.2	829	12	B1907389
11	621.4	28.6	1132	12	BW922650
12	587.6	27.0	768	12	B1837662
13	587.4	27.0	728	10	BG470298
14	566.4	26.0	916	13	BX327159
15	550.2	25.3	940	13	BX327150
16	498.8	22.9	757	14	CD36678
17	491.6	22.6	498	12	BM149841
18	453.8	20.9	479	12	BM148244
19	450.2	20.7	455	12	B1821044
20	401.2	18.4	470	14	CB473966
21	399.6	18.4	494	10	BF601607
22	398	18.3	413	9	AU159990
23	379	17.4	677	10	BG474019
24	361.2	16.6	542	14	CD369993
25	341	15.7	673	12	B1524874
26	338	15.5	638	13	BU241925
27	310.6	14.3	691	13	BQ189982
28	299.2	13.7	956	13	BQ646025
29	299	13.7	650	12	BM389471
30	288	13.2	1226	14	CB961156
31	273.6	12.6	281	10	BE242923
32	269.2	12.4	411	10	BF653124
33	264.4	12.2	364	9	A1334650
34	264.4	12.2	388	9	A1307612
35	255.8	11.8	1033	9	AU090784
36	250.2	11.5	400	9	AM079047
37	237.8	10.9	425	14	CB696535
38	237	10.9	261	13	BX100570
39	232.6	10.7	734	9	AJ398341
40	226.8	10.4	721	14	CB499434
41	213.8	9.8	312	10	AM874319
42	208.2	9.6	920	14	CA489572
43	205	9.4	205	9	A1364431
44	193.8	8.9	824	10	BG758149
45	188.2	8.6	460	14	CB325982

ALIGNMENTS

RESULT 1
BX358485
LOCUS
DEFINITION
BX358485 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1039YL23 5-PRIME, mRNA sequence.
BX358485
ACCESSION
BX358485.1 GI:30378239
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1104)
Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5080.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOD1039C120P1c1cluster=5080.r. Contact: Feng Liang Email: fliang@lifeitech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600

QY 543 CTGACCGCGCTGCTGAGTTCCTCAAAATGATTCATCAAGAGCTGCGGTGAAGACAGC 602
 DB 548 CTGACCGCGCTGCTGAGTTCCTCAAAATGATTCATCAAGAGCTGCGGTGAAGACAGC 607
 QY 603 CTGCTCGGAGAGACAGAGAGCGTGTGCAAGAGGCTCAAGAGAGTGCAGAGCCGCGAGC 662
 DB 608 CTGCTCGGAGAGACAGAGAGCGTGTGCAAGAGGCTCAAGAGAGTGCAGAGCCGCGAGC 667
 QY 663 CGGAGCTCAAGCGCTGCAAGAGAGAACTACGACTGCGCTGCGCTGCGCAACAG 722
 DB 668 CGGAGCTCAAGCGCTGCAAGAGAGAACTACGACTGCGCTGCGCTGCGCAACAG 727
 QY 723 AGTGAAGAGAGAGCGCGCGCTCATGCGGAACCTGACCTGCAAGTGAATTGACAG 782
 DB 728 AGTGAAGAGAGAGCGCGCGCTCATGCGGAACCTGACCTGCAAGTGAATTGACAG 787
 QY 783 CTCAAGCAGACCTCATGAAGAGCGGAGAGCA 814
 DB 788 CTCAAGCAGACCTCATGAAGAGCGGAGAGCA 819

RESULT 4
 BI907340 775 bp mRNA linear EST 16-OCT-2001
 LOCUS 603063637F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212881 5',
 DEFINITION mRNA sequence.

ACCESSION BI907340
 VERSION BI907340.1 GI:16170158
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM1534 row: 1 column: 10
 High quality sequence stop: 772.
 Location/Qualifiers

FEATURES

source

1. 775
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5212881"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

BASE COUNT

161 a 238 c 252 g 124 t

ORIGIN

Query Match 34.6%; Score 752.8; DB 12; Length 775;
 Best Local Similarity 99.0%; Pred. No. 7.8e-13;
 Matches 768; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 4 ATCAGAGAGTGCACAGAGGCTCCGGCGCTCCTCCCTCCCTGAGAGCCCGGAGACATCT 63
 DB 1 ATCAGAGAGTGCACAGAGGCTCCGGCGCTCCTCCCTCCCTGAGAGCCCGGAGACATCT 60
 QY 64 CCCAGAGGCTCCGGCGCCAGAGCTCCTGATGTCTGTCAGAGTGTGCTCTGAGAGA 123
 DB 61 CCCAGAGGCTCCGGCGC-CAGAGCTCCTGATGTCTGTCAGAGTGTGCTCTGAGAGA 119
 QY 124 CCTCAGGCTCCTGCTGAGAGCCATGTGCACTACGAGAAAGATGACAGTGTGGAACG 183
 DB 120 CCTCAGGCTCCTGCTGAGAGCCATGTGCACTACGAGAAAGATGACAGTGTGGAACG 179
 QY 184 TCTGAGAGGCTTCCGGGTGACGCTCACCTGGTTCATGACCCCTCACGATGACACTT 243
 DB 180 TCTGAGAGGCTTCCGGGTGACGCTCACCTGGTTCATGACCCCTCACGATGACACTT 239
 QY 244 ACCTCGGCAATGCAAGGTCTCTGAACCTGATGATGAGAGCAGGTCTCAGGACCCCA 303
 DB 240 ACCTCGGCAATGCAAGGTCTCTGAACCTGATGATGAGAGCAGGTCTCAGGACCCCA 299
 QY 304 ACCTGTATCCGCAAGCAAGAGTGGGTGTCTCTGACATCTCTCAGCGACCGGCC 363
 DB 300 ACCTGTATCCGCAAGCAAGAGTGGGTGTCTCTGACATCTCTCAGCGACCGGCC 359
 QY 364 ACAAGGCTACGTGACCTTCTCTGAGAGCTGAGACTTACTACCCGCAAGCTGTACAGA 423
 DB 360 ACAAGGCTACGTGACCTTCTCTGAGAGCTGAGACTTACTACCCGCAAGCTGTACAGA 419
 QY 424 AGGTCAACAGGCAAGAGAGCGCGCGCTTCTCTCAATGATATGAGCGCTCCGGAGT 483
 DB 420 AGGTCAACAGGCAAGAGAGCGCGCGCTTCTCTCAATGATATGAGCGCTCCGGAGT 479
 QY 484 CAGGCTTACTCAAGTGTGTATGACTGAGCTGAGAGCTGACAGAGTGCAGAGACC 543
 DB 480 CAGGCTTACTCAAGTGTGTATGACTGAGCTGAGAGCTGACAGAGTGCAGAGACC 539
 QY 544 TGACCGGCTGCTGAGCTCCAAAGATGACTTCATCAAGAGCTCGGGTGAAGACAGCC 603
 DB 540 TGACCGGCTGCTGAGCTCCAAAGATGACTTCATCAAGAGCTCGGGTGAAGACAGCC 599
 QY 604 TGCTGCGCAACACCAAGAGAGGTGTGCAAGAGCTCAAGAGAGTGCAGAGCGGACCC 663
 DB 600 TGCTGCGCAACACCAAGAGAGGTGTGCAAGAGCTCAAGAGAGTGCAGAGCGGACCC 659
 QY 664 GCGAGCTCAAGCGCTGCAAGAGAGAACTACGACTGCGCTGCGCTGCGACAGAGA 723
 DB 660 GCGAGCTCAAGCGCTGCAAGAGAGAACTACGACTGCGCTGCGCTGCGACAGAGA 719
 QY 724 GTGAGAGAGAGGCGCGCGCTCATGCGGAACCGTACCTGACGTGAGATTGAC 779
 DB 720 GTGAGAGAGAGGCGCGCGCTCATGCGGAACCGTACCTGACGTGAGATTGAC 775

RESULT 5

BI907352 765 bp mRNA linear EST 05-AUG-2002
 LOCUS AUI42752 Y79AA1 Homo sapiens cDNA clone Y79AA1000827 5', mRNA
 DEFINITION sequence.

ACCESSION AUI42752
 VERSION AUI42752.1 GI:11004273
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 765)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,D., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.

TITLE HRI human cDNA project
 JOURNAL Unpublished
 COMMENT Contact: Takao Isogai

Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source

1..765

Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Y79A1000827"
/cell_type="retinoblastoma"
/cell_line="Y79"
/clone_lib="Y79A1"
/note="Vector: pME18SFL3"
/note="236 c 242 g 123 t 4 others"

BASE COUNT 160 a 236 c 242 g 123 t 4 others

ORIGIN

Query Match 33.3%; Score 725.4; DB 9; Length 765;
Best Local Similarity 99.0%; Pred. No. 1e-125;
Matches 759; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY 1 ATCATCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCCCGGAGCA 60
DB 1 ATCATCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCCCGGAGCA 60
QY 61 TCTCCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCGTGTCTCTG 120
DB 61 TCTCCAGAGAGTGCACAGGCGTCCGCGCTCCTCCCTCCCTGAGCGTGTCTCTG 120
QY 121 AGACCTCTGAGCTGCTGCTGAGGCGTCTGAGCTGAGCTGAGCTGAGCTGAG 180
DB 121 AGACCTCTGAGCTGCTGCTGAGGCGTCTGAGCTGAGCTGAGCTGAGCTGAG 180
QY 181 AGCTCTGAGAGGCTTCCGGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 240
DB 181 AGCTCTGAGAGGCTTCCGGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 240
QY 241 CTTACCTGAGGCGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 300
DB 241 CTTACCTGAGGCGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 300
QY 301 CCAACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 360
DB 301 CCAACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 360
QY 361 GCCACAAAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 420
DB 361 GCCACAAAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 420
QY 421 AGAAGTTCAGAGGCGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 480
DB 421 AGAAGTTCAGAGGCGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 480
QY 481 AGTGAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 540
DB 481 AGTGAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 540
QY 541 ACCTGACCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 600
DB 541 ACCTGACCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 600
QY 601 GCTGCTGCGAGAGCAGAGAGCTGAGAGCTCAAGAGAGAGTGGAGAGCGGCA 660
DB 601 GCTGCTGCGAGAGCAGAGAGCTGAGAGCTCAAGAGAGAGTGGAGAGCGGCA 660
QY 661 GCCGCGAGCTCAAGAGAGCTGAGAGAGTCAAGAGAGTGGAGAGCGGCA 720

DB 661 GCCGCGAGCTCAAGAGAGCTGAGAGAGTCAAGAGAGTGGAGAGCGGCA 718
QY 721 AGAGTGAAGAGAGAGGCGCGCGC-TCATGCGAGAGCTGACCTGCA 766
DB 719 AMAATGAGAGAGAGGCGCGCGCTTCATGCGAGAGCTGACCTGCA 765

RESULT 6

LOCUS

B1905841 722 bp mRNA linear EST 16-OCT-2001

DEFINITION

603062919P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212037 5',

ACCESSION

B1905841

VERSION

B1905841.1

KEYWORDS

EST

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 722)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/MLN at:

<http://image.llnl.gov>

Plate: L14M1532 row: f column: 06

High quality sequence stop: 714.

Location/Qualifiers

1..722

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5212037"

/tissue_type="leukocyte"

/lab_host="DH10B"

/clone_lib="NIH_MGC_118"

/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV

(destroyed); RNA source leukocytes from anonymous pool of

non-activated adult donors. Library is oligo-dT primed

and directionally cloned (BcoRV site is destroyed upon

cloning). Average insert size 1.7 kb. Insert size range

1.2-3.3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:

this is a NIH_MGC Library."

BASE COUNT 156 a 216 c 233 g 117 t

ORIGIN

Query Match 32.1%; Score 689; DB 12; Length 722;
Best Local Similarity 99.7%; Pred. No. 8.9e-121;
Matches 721; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 80 CCCAGGCTCTGGTGTGTGTGAGTGCAG-GTGGCTCTGGAAGACCTTCAAGCTGCTG 138
DB 1 CCCAGGCTCTGGTGTGTGTGAGTGCAGTGTGGCTCTGGAAGACCTTCAAGCTGCTG 60
QY 139 CTGAGGCCATGTGCGAGCTACGAGGAGTGAAGTGAAGTGTGAGGAGGCTTCC 198
DB 61 CTGAGGCCATGTGCGAGCTACGAGGAGTGAAGTGAAGTGTGAGGAGGCTTCC 120
QY 199 GGGTGAAGCTCACTTCGCTGATGAGCCCTTCAAGCTTCACTTCACTTCACTTCA 258
DB 121 GGGTGAAGCTCACTTCGCTGATGAGCCCTTCAAGCTTCACTTCACTTCACTTCA 180
QY 259 AGGTCTGAAGCTTATGATGATGAGAGAGTGTGAGGAGAGCCCAAGCTGATCATCGCA 318

Db 181 AGGTCCTGAACCTGTATGATGAGAGAGGTGTCTCAGCGACCCCAACCTGTATCCGCA 240
 QY 319 AACGAAAGTGGTGTGTCTCTCTGACATCTCTGACGCGACCCGCAAGAGGCTACGTGG 378
 Db 241 AACGAAAGTGGTGTGTCTCTCTGACATCTCTGACGCGACCCGCAAGAGGCTACGTGG 300
 QY 379 CCTTCTCGAGACCTCTGAGCTTCTAATCCCGAGCTGTATCAGAGAGTCAAGAGGCAAG 438
 Db 301 CCTTCTCGAGACCTCTGAGCTTCTAATCCCGAGCTGTATCAGAGAGTCAAGAGGCAAG 360
 QY 439 AGCGGCGCGCGCTCTCTCTGATATGATGACGCGCTCCGAGAGTCAAGGCTGACTCAGC 498
 Db 361 AGCGGCGCGCGCTCTCTCTGATATGATGACGCGCTCCGAGAGTCAAGGCTGACTCAGC 420
 QY 499 TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 558
 Db 421 TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 559 GCTTCAAAAGTGAATCTTATCAAGAGTGTGGGTGAAGACAGCTGTGTGCGAAGCACC 618
 Db 481 GCTTCAAAAGTGAATCTTATCAAGAGTGTGGGTGAAGACAGCTGTGTGCGAAGCACC 540
 QY 619 AGAGAGCTGTGAGAGGCTCAAGAGAGTGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 678
 Db 541 AGAGAGCTGTGAGAGGCTCAAGAGAGTGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 600
 QY 679 GCAAG 738
 Db 601 GCAAG 660
 QY 739 CCGGCTCATGCGGAGACCTGACCTGACGCTGAGATGACAGCTCAAGACAGAGCTCA 798
 Db 661 CCGGCTCATGCGGAGACCTGACCTGACGCTGAGATGACAGCTCAAGACAGAGCTCA 719
 QY 799 TGA 801
 Db 720 TGA 722

RESULT 7
 BI912159 755 bp mRNA linear EST 16-OCT-2001
 LOCUS 60306408F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214576 5',
 DEFINITION mRNA sequence.
 ACCESSION BI912159
 VERSION BI912159.1 GI:16176140
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 755)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LHAM1538 row: P column: 01
 High quality sequence stop: 689.
 Location/Qualifiers
 1..755
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5214576"
 /rseq_type="leukocyte"

/lab host="DH10B"
 /clone.lib="NIH_MGC_118"
 /note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is inserted upon
 cloning). Average insert size 1.7 kb. Insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH MGC Library."

BASE COUNT 157 a 231 c 246 g 121 t
 ORIGIN

Query Match 30.7%; Score 668; DB 12; Length 755;
 Best Local Similarity 97.3%; Pred.No. 5,7e-115;
 Matches 732; Conservative 0; Mismatches 15; Indels 5; Gaps 5;

Db 52 CGGAGAGATCTCCAGAGGCTCCGCGGCCAGAGCTCTGTGTGTCTGACAGTGAAGTGTG 111
 5 CGGAGAGATCTCCAGAGGCTCCGCGGCCAGAGCTCTGTGTGTCTGACAGTGAAGTGTG 63
 QY 112 GCTCTGAGAG-ACCCTGAGCTGCTGAGAGCAATGTGAGACTAGAGAGATGATGAC 170
 Db 64 GCTCTGAGAGAGCTCTGAGCTGCTGAGAGCAATGTGAGACTAGAGAGATGATGAC 123
 QY 171 GAGTCTGAGAGAGCTCTGAGAGGCTTCCGAGTGAAGCTCACTGAGTCACTGAGTCA 230
 Db 124 GAGTCTGAGAGAGCTCTGAGAGGCTTCCGAGTGAAGCTCACTGAGTCACTGAGTCA 183
 QY 221 CGCATCAACCTTACCTGAGAGTGAAGTCTGAACTGATGATGAGAGAGAGTGTG 290
 Db 184 CGCATCAACCTTACCTGAGAGTGAAGTCTGAACTGATGATGAGAGAGAGTGTG 243
 QY 291 CTCAG 350
 Db 244 CTCAG 303
 QY 351 CAGCGAG 410
 Db 304 CAGCGAG 363
 QY 411 CAGCTGTACAGAGAGTCAAG 470
 Db 364 CAGCTGTACAGAGAGTCAAG 422
 QY 471 GCGTCGAGAGAGTCAAG 530
 Db 423 GCGTCGAGAGAGTCAAG 482
 QY 531 AAGGTGACAGAGAGTCAAG 590
 Db 483 AAGGTGACAGAGAGTCAAG 542
 QY 591 GTGAAGAGAGAGCTGAG 650
 Db 543 GTGAAGAGAGAGCTGAG 602
 QY 651 GAGGCGAG 710
 Db 603 GAGGCGAG 661
 QY 711 TGAGGCGAG 770
 Db 662 TGAGGCGAG 721
 QY 771 GAG-ATTGACAG 801
 Db 722 GAGCATTGACAG 753

RESULT 8
 BX38484/c

LOCUS	BX358484	1091 bp	mRNA	linear	EST 05-MAY-2003
DEFINITION	BX358484 Homo sapiens placenta COT 25-NORMALIZED Homo sapiens CDNA clone CSODI039YL23 3-PAlME, mRNA sequence.				
ACCESSION	BX358484				
VERSION	BX358484.1	GI:30376237			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1. (bases 1 to 1091)				
JOURNAL	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
COMMENT	Full-length cDNA libraries and normalization unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5080.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI039CF12NP&cluster=5080.r . Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI039CF12NP. Location/Qualifiers 1..1091 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODI039YL23" /issue_type="PLACENTA COT 25-NORMALIZED" /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-cligc(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."				
BASE COUNT	153 a	356 c	322 g	237 t	23 others
ORIGIN					
Query Match	29.9%; Score 650.4; DB 13; Length 1091;				
Best Local Similarity	76.5%; Pred. No. 1,2e-111;				
Matches	941; Conservative	19; Mismatches	44; Indels	226; Gaps	5;
Db	999 GAGGACTGGCGGCAGGCGCTGGCGGAGCAACCAGAGCAGAGGCCAACCATCTTCTCCCTG	1078 GRRGAGASTGGCGCAGGSGTGCCGAGCACACGAGGCRAGCCAAACGATCTTCGCTG	1013A		
Gy	1059 CGCAGAGACCTTCGCCAGAGGCGCGCCGACGCGCTCCGTGATGAGAGAAGAGAGT	1118B			
Db	1018 SGCAAGAGACSTCCGCGCAGGCGCAGGCGCCGAC-SCTCGGTGATGAGAGAAGAGATG	960			
Gy	1119 TTGAGCTGAGCTGCTGCTGCACTAGTAAGAGCTCCAAGTATGAAGGACCGCATCGAG	1178E			
Db	959 TTCGAGCTGCACTSCCTGGCA--TAGTAAAGCTCCAAAGTTATPAAAGACCGCATCGAG	902			
Gy	1179 GCCATCTGCTCTCAATATGAGAGAGGCTGCGCATTTGAGCGGACCAAGACACAATAATGAG	1238F			
Db	901 GCCATCTGCKKCAAGATGAGAGAGGTCCGCAATTGAGCGGAC-----	860			
Gy	1239 GGGCTGTGACCAAGCCTCCGCGGCCACAGCGGCTTGAAGCTCTCGAGGACCTCTGCTTGAAGT	1298G			
Db	859 -----	860			
Gy	1299 TGGGCGGCGGCGCCAGAGGCGCCAGGCGAAGCTTTGGGGCCCTCACTGAGGAGTGGCCTTGT	1355H			
Db	859 -----	860			
Gy	1359 GGTGTCCTCGTCAAGGCATGACACGCGGGAGAGGTGACAGACACGACGCCCCGGGGCCT	1411I			
Db	859 -----	860			
Gy	1411 CAAGGCTATGACACGCGGGAGATTTTTTKACGACACGACACGCCCCGGGGCCT	810			

[illegible]

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LIML1538 row: F column: 15
High quality sequence start: 9
High quality sequence stop: 732.

FEATURES

SOURCE

1. 738
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5214350"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_id="NIH_MGC_118"
/note="Vector: PCMV-SPORE6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT

151 a 225 c 243 g 119 t

ORIGIN

Query Match 29.7%; Score 645.6; DB 12; Length 738;
Best Local Similarity 97.5%; Pred. No. 8.7e-111;
Matches 698; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

24 CCGGCGGCTCTCCCTCCCTCCGAGAGCCCGGAGAGATCTCCAGAGAGCTCCGCGGCCA 83
23 CGGTCGTCT 82
84 GGC-TTCCTGCTGTCT 141
83 GGGCTCTGT 142
142 AGGCTATGTGGAGTACGAGAGATGACAGTGTCTGGAAGTCTCTGGAAGGCTTCCGGG 201
143 AGGCTATGTGGAGTACGAGAGATGACAGTGTCTGGAAGTCTCTGGAAGGCTTCCGGG 202
202 TGAAGCTCACTGGT 261
203 TGAAGCTCACTGGT 262
262 TCTCTGAAGCTGTATGATGAGAGAGAGTGTCTACGAGAGAGAGAGAGAGAGAGAGAG 321
263 TCTCTGAAGCTGTATGATGAGAGAGAGTGTCTACGAGAGAGAGAGAGAGAGAGAGAG 322
322 GGAAGTGGTGTGTCT 381
323 GGAAGTGGTGTGTCT 382
382 TCTCTGAAGCTGTATGATGAGAGAGAGTGTCTACGAGAGAGAGAGAGAGAGAGAGAG 441
383 TCTCTGAAGCTGTATGATGAGAGAGTGTCTACGAGAGAGAGAGAGAGAGAGAGAGAG 442
442 CCGGCGGCT 501
443 CCGGCGGCT 502
502 TGAATGATGAGTCTATGAG 561
503 TGAATGATGAGTCTATGAG 562

QY

562 CCAAGATGATCTTATCAAGAGAGCTGCGGTGAAAGACAGAGCTGTGCGAAGACAGG 621

Db

563 CCAAGATGATCTTATCAAGAGAGCTGCGGTGAAAGAGAGAGCTGTGCGAAGACAGG 622

QY

622 AGCGTGTCCAGAGAGCTCAA-GAGAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 680

Db

623 AGCGTGTCCAGAGAGCTCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 682

QY

681 AAGAGAGAGAA-CTACGAGCTTGCGCATGCGCTGCGGACCAAGAGTGAAGAGAGG 735

Db

683 ACGAGAGAGAACTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 738

RESULT 10

BF307399 829 bp mRNA linear EST 21-NOV-2000
LOCUS 601894035F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139529 5',
DEFINITION mRNA sequence.

ACCESSION

BF307399.1 GI:11254514

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS

1 (bases 1 to 829)
NIH-MGC http://mgi.nci.nih.gov/.

TITLE

Unpublished

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

FEATURES

Location/Qualifiers

source

1. 829
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4139529"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_17"
/note="Organ: muscle; Vector: pOT87; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGATCAGC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

173 a 249 c 279 g 128 t

ORIGIN

Query Match 29.2%; Score 636.2; DB 10; Length 829;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 707; Conservative 0; Mismatches 63; Indels 3; Gaps 3;

QY

6 CAGAAAGTGCACAGAGAGCTCCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 65

Db

2 CAGAAAGTGCACAGAGAGT-CGGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60

QY

66 CAGAGGCTCCGCGGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125

Db

61 CAGAGGCTCCGCGG-CAGAGGCTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 119

QY

126 CTCAGCTGCTGCTGAGAGAGATGCGAGTACGAGAGAGATGAGAGTGTGGAAGCTC 185

Db 120 CTGACGCTGCTGCTGAGGCGCATGTGCGACTAGAGAAAGATGAGACGAGTGTGAGAGCTTC 179
QY 186 CTGAGAGGCTTCCGGGTGAGAGCTCACTCGGTGATGACCCCTCAAGCATCAACCTTAC 245
Db 180 CTGAGAGGCTTCCGGGTGAGAGCTCACTCGGTGATGACCCCTCAAGCATCAACCTTAC 239
QY 246 CTGCGGAGTGAAGAGTCTTGAACCTGATGATGAGAGAGAGTGTCTAGACCCCAAC 305
Db 240 CTGCGGAGTGAAGAGTCTTGAACCTGATGATGAGAGAGAGTGTCTAGACCCCAAC 299
QY 306 CTGCTCACTCGCAAGAGAGTGGTGTCTCTGAGCATCTCTGAGAGAGAGAGAGAGAG 365
Db 300 CTGCTCACTCGCAAGAGAGTGGTGTCTCTGAGCATCTCTGAGAGAGAGAGAGAGAG 359
QY 366 AAGGGCTACGCTGAGCTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
Db 360 AAGGGCTACGCTGAGCTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
QY 426 GTCAAG 485
Db 420 GTCAAG 479
QY 486 GGGCTGACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 545
Db 480 GGGCTGACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 539
QY 546 ACCGCGCTGCTGAGCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATG 605
Db 540 ACCGCGCTGCTGAGCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATG 598
QY 606 CTGCGCAAG 665
Db 599 GTGCGCAAG 658
QY 666 GAGCTCAAG 725
Db 659 AGCTCAAG 718
QY 726 GAG 778
Db 719 CGAG 771

RESULT 11
BM922630 1132 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6652616 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5755714
DEFINITION 5', RNA sequence.
ACCESSION BM922630
VERSION BM922630.1 GI:19373009
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catartini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1132)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC).
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM2795 row: c column: 11
High quality sequence stop: 592.
Location/Qualifiers
1. 1132

FEATURES
source
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/db_xref="taxon:9606"
/clone="IMAGE:5755714"
/tissue_type="leukocyte"
/lab_host="MDH10B"
/clone_id="NIH_MGC_118"
/note="Vector: pCMV-SPORT6, Site_1: NotI, Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH MGC Library."
BASE COUNT 243 a 363 c 331 g 195 t
ORIGIN

Query Match 28.6%; Score 621.4; DB 12; Length 1132;
Best Local Similarity 98.0%; Pred. No. 3.2e-106;
Matches 650; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 44 TGCACCCCGGAGACATCTTCCAGAGAGCTCCGCGGCCAGGCTCTGCTGTGTCTGAG 103
Db 20 TGCACCCCGGAGACATCTTCCAGAGAGCTCCGCGGCCAGGCTCTGCTGTGTCTGAG 79
QY 104 TGCAGAGTGTCTCTGAG 163
Db 80 TGCAGAGTGTCTCTGAG 139
QY 164 CGATGAGAGTGTCTGAG 223
Db 140 CGATGAGAGTGTCTGAG 199
QY 224 CCCCTCAAGCATCAACCTTACTCTGCGAGAGTGAAGTCTGGAACCTGATGAGAGAG 283
Db 200 CCCCTCAAGCATCAACCTTACTCTGCGAGAGTGAAGTCTGGAACCTGATGAGAGAG 259
QY 284 GCAAGTGTCTGAG 343
Db 260 GCAAGTGTCTGAG 319
QY 344 CATCTGAG 403
Db 320 CATCTGAG 379
QY 404 CTACCCGAGAGTGTCAAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
Db 380 CTACCCGAGAGTGTCAAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 439
QY 464 CATGCAAGAGTGTGAG 523
Db 440 CATGCAAGAGTGTGAG 499
QY 524 GCAAGAGAGTGTGAG 583
Db 500 GCAAGAGAGTGTGAG 559
QY 584 GCTGCGGTGAG 643
Db 560 GCTGCGGTGAG 619
QY 644 GAG 701
Db 620 GAG 679
QY 702 GCC 704
Db 680 GGC 682

RESULT 12
B1837662

LOCUS B1837662 768 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603086501F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5225377 5',
 mRNA sequence.
 ACCESSION B1837662
 VERSION B1837662.1 GI:15949212
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 768)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L14M1567 row: b column: 02
 High quality sequence stop: 707.
 Location/Qualifiers
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 /clone="IMAGE:5225377"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_120"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH_MGC Library."
 BASE COUNT 174 a 229 c 258 g 107 t
 ORIGIN
 Query Match 27.0%; Score 587.6; DB 12; Length 768;
 Best Local Similarity 94.4%; Pred. No. 6,2e-100;
 Matches 719; Conservative 0; Mismatches 29; Indels 14; Gaps 10;

590 GGTGAAGACAGCC-TGCTGCCAA-GCACAGAGGCTGCAAGGCTCAAGAGAG 647
 361 GGTGACGCGCAGCTTGTCTGCAATGACACAGAGGCTGTGAGAGGCTCAAGAGAG 420
 648 TGCAGAGCCGAGCA-GCCGAGAGCTCAAGGCTGCAAGAGAGCACTAGGCTG 706
 421 TGCAGAGCCGAGCATGCTCCGAGAGCTCAAGGCTGCAAGAGAGCACTAGGCTG 480
 707 GCGCTGCGCAGCAGAGTGAAGAGAGAGGCGCGC-GCTCATGCGGA-CCGTGACTG 764
 481 GCGCTGCGCAGCAGAGTGAAGAGAGAGGCGCGC-GCTCATGCGGA-CCGTGACTG 540
 765 CAGCTGGAAGATTGACCAAGCTCAAGCAGAGCTCAAGAGCCGAGAGCACTGCAAGT 824
 541 CAGCTGGAAGATTGACCAAGCTCAAGCAGAGCTCAAGAGCCGAGAGCACTGCAAGT 600
 825 GAGGCG-----AGCACAGCTGAAGCTCAGGCAC-GCCATGAGCA-GGCGCCAGCCA 877
 601 GGAAGCCGAGACACAGCTGCAAGCTCAGGCACGCGCATGAGAGAGGAGAGCAAGCA 660
 878 GAGCTGCTGTGGAGCTGAGAGAGAGAGAGAGGCGCTGCTCAAGCCCGGAGTGAAGCT 937
 661 GAGCTGCTGTGGAGCTGAGAGAGAGAGAGAGGCGCTGCTCAAGCCCGGAGTGAAGCT 720
 938 GAGGCGCTGCTGCTGAGAGAGAGAGAGAGAGGCGCTGCTCAAGCCCGGAGTGAAGCT 979
 721 GAGGCGCTGCTGCTGCA-GAGGAGAGCTGAGACAGAGAGAGAGCC 761

RESULT 13
 BG470298 728 bp mRNA linear EST 21-MAR-2001
 BG470298
 LOCUS 602533257F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660886 5',
 mRNA sequence.
 ACCESSION BG470298
 VERSION BG470298.1 GI:13402573
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 728)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L10M1459 row: a column: 15
 High quality sequence stop: 667.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:4660886"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_15"
 /note="Organ: colon; Vector: pOTB1; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 171 a 207 c 258 g 92 t
ORIGIN

Query Match 27.0%; Score 587.4; DB 10; Length 728;
Best Local Similarity 96.8%; Pred. No. 6,7e-100;
Matches 696; Conservative 0; Mismatches 11; Indels 12; Gaps 9;

QY 461 GATCATCGAGCGCTCGGGGAGTCAAGCCCTGATCTAGCTCTGATGATGAGTCTATGA 520
DB 2 GATCATCGAGCGCTCGGGGAGTCAAGCCCTGATCTAGCTCTGATGATGAGTCTATGA 61
QY 521 GCTGCGAAGAAGGTGCGAGGACCTGACCGCGCTGAGAGTCCAAAGATGACTTCACAA 580
DB 62 GCTGCGAAGAAGGTGCGAGGACCTGACCGCGCTGAGAGTCCAAAGATGACTTCACAA 121
QY 581 GGAAGCTGCGGGTGAAGGACAGCTGTCTGCCAAGACACAGAGCGTGTGCGAGGCTCAA 640
DB 122 GGAAGCTGCGGGTGAAGGACAGCTGTCTGCCAAGACACAGAGCGTGTGCGAGGCTCAA 181
QY 641 GGAAGAGTGCAGAGCCGCGAGCCGCGAGCTCAAAGCGTGCAGAGAGAGAACTACGACCT 700
DB 182 GGAAGAGTGCAGAGCCGCGAGCCGCGAGCTCAAAGCGTGCAGAGAGAGAACTACGACCT 241
QY 701 GCGCATCGCTGCGGCGACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
DB 242 GCGCATCGCTGCGGCGACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 761 CCTGCGAGTGAAGATTGACAGAGTCAAGACAGCTCTCATAGAGCGGAGAGACATGCAA 820
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QY 821 GATGAGAGCGGAGACAGAGCTGAAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 880
DB 362 GATGAGAGCGGAGACAGAGCTGAAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
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QY 940 AGGCTTCCTGTCAG 996
DB 482 AGGCTTCCTGTCAG 541
QY 997 -AGGAGAGAGTGGGGGAG 1053
DB 542 AAGAGAGAGTGGGGGAG 601
QY 1054 CCTGCGCAA--GGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
DB 602 CCTGCGCAAAG 661
QY 1111 AGGAGATGTTG-AGCTGAGAGTGCCTTGCA-CTAAGTAAAGACTCCAAAGTGTACAG 1167
DB 662 AGGAGATGTTGAGAGAGTGCCTTGCAAGTAAAGAGTCCAAAGTGTACAGAG 720

RESULT 14
BX327159 916 bp mRNA linear EST 02-MAY-2003
LOCUS BX327159 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI039Y123 5-PRIME, mRNA sequence.
ACCESSION BX327159
VERSION BX327159
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polaves, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5080.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF025ZB10_AF02379_2&cluster=5080.r.
Contact : Feng Liang Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAF025ZB10_AF02379_2.
Location/Qualifiers
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI039Y123"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 196 a 279 c 328 g 105 t 8 others
ORIGIN

Query Match 26.0%; Score 566.4; DB 13; Length 916;
Best Local Similarity 82.0%; Pred. No. 6e-96;
Matches 775; Conservative 0; Mismatches 18; Indels 152; Gaps 5;

QY 920 GGGCCGGGTGCAAGAGCTGAGAGCTCCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979
DB 13 GGGCCGGGTGCAAGAGCTGAGAGCTCCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 71
QY 980 CTACATCCAGGTAATGAG 1039
DB 72 CTACATCCAGGTAATGAG 131
QY 1040 CAACACATCTTCTCCGCGAG 1099
DB 132 CAACACATCTTCTCCGCGAG 191
QY 1100 CATGAG 1159
DB 192 CATGAG 251
QY 1160 GTACAAAGACCGCATGAG 1219
DB 252 GTACAAAGACCGCATGAG 311
QY 1220 CCAGAGACACAAATGAG 1279
DB 312 C----- 312
QY 1280 CCGAGCTCTGCTTGGAGTGGGGCGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
DB 313 ----- 312
QY 1340 CACTGAGAGTGGCTTGGAGTGGCTCCGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
DB 313 -----CAGGCATAGCCACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
QY 1400 CACAGACGCGCGGGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
DB 344 CACAGACGCGCGGGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
QY 1460 GCGAGAGAGCGAGTGAAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
DB 404 GCGAGAGAGCGAGTGAAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
QY 1520 TGGAGGAGAGGCTCAAG 1579
DB 464 TGGAGGAGAGGCTCAAG 523

[illegible]

RESULT 15	
LOCUS	BX327160
DEFINITION	BX327160 Homo sapiens 940 bp mRNA, linear, EST 02-MAY-2001
ACCESSION	BX327160
VERSION	BX327160
KEYWORDS	clone CSOD1039YLT3 5-PRIME, mRNA sequence.
SOURCE	BX327160
ORGANISM	BX327160.1 GI:30346483
	EST.
	Homo sapiens (human)
	Homo sapiens
	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1. (bases 1 to 940)
AUTHORS	L.I. W.B., Gruber, C., Jesssee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	unpublished
COMMENT	Contact: Genoscope

BASE COUNT	202 a	293 c	331 g	112 t	2 others
ORIGIN					

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976  GCCCCTCATATCCAGGATCTGTGAGAGGAGATCTGCGCGCAGGCGCTCCGGGACCAACCAAGAGGC 103
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Db    126 AGGCGCAACACCATTTTCTCCCTCGGCAAGGACCTCCGCGAGGCGAGGCCGACGCTCC 185
QY    1096 GGTGTCATGAGAGAGAGAGAGATGTTTCAGCTGCAGTGCCTTGGCACTACGTAAAGACTTCCA 1155
Db    186 GGTGTCATGAGAGAGAGAGAGATGTTTCAGCTGCAGTGCCTTGGCACTACGTAAAGACTTCCA 245
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QY    1396 CACGCACAGACACGCCCGGGGCTGTGCAGAGAGAGAGCGGCTGCGCAAGCAGGTGCGGAG 1455
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QY    1456 CTGGGCGAAGAAAGCGGATGAGCTTGCAGCTGCAGTGTTCAGTGTGAGCGCAGACTACTG 151.5
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QY    1516 GCCGTGAGAGGGCAGGCTCAGGCGGCGACAGCTGAGAGACGCTGCTCTGAGTCCGACTG 1575
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QY    1576 GAAGATGAGCTCACCCAGAGAGGTCCAGAGAGCTCATCTCCGCCAGAGACTGTGAGAGACAC 1635
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QY    1636 CAGCTCTCAGACAAAGGCTGCTTGGCGCGCGGCGGAGACCCGAAACAGCCTTTTGACACT 1695
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QY    1696 CTGCACAGAGACAGGTTTTCGGAACCCCCATGACGAGGCTTGAGCAGCGGGGAGCG 1755
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QY    1756 CCCGAGAGAGAGCGCGCGCGCTCTTAAGAGAGTTTGTGAACCTACCGCAGAGAGCGCGCC 1811.5
Db    698 CCCGAGAGAGAGCGCGCGCGCTC--AAGAGAGTTTGTAG-----ACTACCGCAGAGAGCGCG 752
QY    1816 CTACGAGAGAGATGCAGAAAGAGATGCGCGCAGGGGAGAGAGACCGGAGAGAC 1866
Db    753 CCTCAGAGAGATGC--AAAAAGATGCGCCGACAGTGAAGAGACCGGAGAGACAC 801

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2004, 09:51:41 ; Search time 146 Seconds
(without alignments)
6578.423 Million cell updates/sec

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Perfect score: 2176
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132.8	6.1	9551	1	US-08-056-200-93 Sequence 93, Appl
2	132.8	6.1	9551	2	US-08-800-644-93 Sequence 93, Appl
3	101	4.6	3489	2	US-08-728-323A-1 Sequence 1, Appl
4	101	4.6	3489	4	US-09-298-568-1 Sequence 1, Appl
5	101	4.6	3489	4	US-09-410-399-1 Sequence 1, Appl
6	101	4.6	32207	2	US-08-770-379-20 Sequence 20, Appl
7	101	4.6	32207	4	US-08-757-669A-20 Sequence 20, Appl
8	101	4.6	32207	4	US-09-330-371A-20 Sequence 20, Appl
9	100.6	4.6	1926	4	US-09-249-585A-2 Sequence 2, Appl
10	100.6	4.6	1926	4	US-09-410-399-3 Sequence 3, Appl
11	100.6	4.6	2580	4	US-09-050-863-2 Sequence 2, Appl
12	100.6	4.6	2580	4	US-09-359-081-2 Sequence 2, Appl
13	100.6	4.6	5452	2	US-09-130-114-1 Sequence 1, Appl
14	100.6	4.6	8705	4	US-09-647-344A-14 Sequence 14, Appl
15	100.6	4.6	9600	4	US-08-910-647-1 Sequence 1, Appl
16	100.6	4.6	9600	4	US-09-620-925-1 Sequence 1, Appl
17	100.6	4.6	10596	1	US-07-884-811-15 Sequence 15, Appl
18	100.6	4.6	10596	1	US-07-885-971-15 Sequence 15, Appl
19	100.6	4.6	10596	1	US-08-087-783A-15 Sequence 15, Appl
20	100.6	4.6	10596	1	US-08-194-088B-15 Sequence 15, Appl
21	100.6	4.6	10596	2	US-08-194-087-15 Sequence 15, Appl
22	100.6	4.6	10596	2	PCT-US93-04648-15 Sequence 3, Appl
23	90	4.1	1185	3	US-09-023-339-3 Sequence 3, Appl
24	90	4.1	1260	3	US-09-023-173-5 Sequence 5, Appl
25	90	4.1	1308	3	US-09-023-173-10 Sequence 10, Appl
26	90	4.1	1308	3	US-09-023-339-6 Sequence 6, Appl
27	88.4	4.1	1995	1	US-08-425-069-3 Sequence 3, Appl

28	88.4	4.1	1995	2	US-08-317-844B-3	Sequence 3, Appl
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36	73.6	3.4	1926	4	US-09-249-585A-4	Sequence 4, Appl
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38	67.2	3.1	2793	1	US-08-209-747-1	Sequence 1, Appl
39	67.2	3.1	2793	1	US-08-458-298-1	Sequence 1, Appl
40	63.8	2.9	5651	4	US-08-938-105-2	Sequence 2, Appl
41	63.2	2.9	756	1	US-08-642-255-50	Sequence 50, Appl
42	62.4	2.9	1310	4	US-09-047-288-1	Sequence 1, Appl
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44	62.4	2.9	2180	3	US-09-286-904-23	Sequence 23, Appl
45	62.4	2.9	2180	4	US-09-640-101-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-056-200-93
Sequence 93, Application US/08056200
Patent No. 5616500
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichopolylin and Transglutaminase-3 and
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056, 200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1507..1644
FEATURE:
NAME/KEY: intron

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1507..1644
FEATURE:
NAME/KEY: Intron
LOCATION: 1645..2511
FEATURE:
NAME/KEY: CDS
LOCATION: 2512..8070
US-08-800-644-93

Query Match 6.1%; Score 132.8; DB 2; Length 9551;
Best Local Similarity 46.9%; Pred. No. 6.1e-18;
Matches 637; Conservative 0; Mismatches 692; Indels 29; Gaps 6;

QY 477 GGGGAGTCAGGCTGACTCAGCTGCTGATGATGAGTCTGAGCTGCAAGAAAGAGTG 536
DB 3190 GAGAGAGAGAGAGAGCTACCGAAGCTGAGCGGCAAGAGCTGAGAGAGAGCGCCAGAG 3249
QY 537 CAGGAGCTGACCGGCTGCTGAGCTGCAAGATGACTTCACTCAAGAGCTGCGGGTGAAG 596
DB 3250 GAAAGAGAGAGAGAGAGAGAGCTGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 3309
QY 597 GAGAGCTGCTGCGCAAG 656
DB 3310 GAG 3369
QY 657 GAG 716
DB 3370 GAG 3429
QY 717 CACCAAG 776
DB 3430 CCGAG 3489
QY 777 GAGCAGCTCAG 836
DB 3490 CCGAG 3549
QY 837 ACCTGAGAGCTCAG 896
DB 3550 GAGCAG 3609
QY 897 CAGCAG 956
DB 3610 CAGGTGAG 3669
QY 957 GGGAGCTGAG 1016
DB 3670 AGGCGCAG 3729
QY 1017 CTGCGGAG 1076
DB 3730 CAGCAG 3786
QY 1077 GAGCAG 1136
DB 3787 GAG 3846
QY 1137 GCACTAGTAAAG 1196
DB 3847 AAG 3906
QY 1197 GAG 1248
DB 3907 GAG 3966
QY 1249 CAGGCTCGGAG 1308

DB 3967 GAG 4026
QY 1309 GAGCAG 1368
DB 4027 AG 4086
QY 1369 CAGGCTAG 1428
DB 4087 GAG 4143
QY 1429 GAGCAG 1488
DB 4144 GAG 4203
QY 1489 GTGTTCCAGTGTGAG-----GCGAGCTTACTGCGCGCTGAGAGAGAGAGAGAGAGAG 1542
DB 4204 CCGAG 4263
QY 1543 CAGCTGAG 1602
DB 4264 CAG 4323
QY 1603 GAGCTCTGACTCCCGCAG 1655
DB 4324 GAGCTGCTGAG 4383
QY 1656 CTTGCGCGAG 1713
DB 4384 CAG 4443
QY 1714 TTGCGGAAAG 1773
DB 4444 CTGAAG 4503
QY 1774 CGCTCAAG 1811
DB 4504 CAGGCTCGGAG 4541

RESULT 3

US-08-728-323A-1
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Behenzky, Roy A.
; APPLICANT: Russo, James U.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,323A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

Db	2109	GGATGAGCAGGAGCAGGATGAGCAGAGCAGAGGATGAGCAGCAGCATGAGCA	2168
Qy	911	CTTCTCCAGGCCCCGGGTGCAGAGCTGAGAGCCTCCGTCCAGAGGGGAAAGCTTGACAG	970
Db	2169	GCAGCAGCAGGATGAGCAGCAGCAGCAGAGATGACAGCAGCAGCAGCATGAGCAGCAGCA	2228
Qy	971	GAGCAGCCCCCAATCCAGGTACTCTGAGAGAGATCTGGCGGAGAGGCGCTGCGCGACACCA	1030
Db	2229	GCAGGATGAGCAGCAGCAGCAGATGAAACAGACACAGAGGAGAGCAGAGCAGCAGCA	2288
Qy	1031	GGACGAGGCCAACCAATCTTCTCTCCGCGAAGAACTCCGCGAGGCGAGGCCAGC	1090
Db	2289	GGAGCAGAGCAGAGATTAGAGAGCAGAGCAGAGCATGTA-----GAGATCAGGA	2339
Qy	1091	CTTCGCGTGCAATGAGAGAAAGAGATGTTGAGCTGCAGTCCCTGGCATTACGTAAGA	1150
Db	2340	GCAGAGATTAGAGGAGCAGAGCAGAGATTAGAGAGAGCAGAGCATGAGATTAGAGAGCA	2399
Qy	1151	CTCCAGATGTACAAAGACCCGCATGAGGCCATCCTCTGCATATGAGAGGTTGCCAT	1210
Db	2400	GGAGCAGAGATTAGAGGAGCAGAGCAGAGATTAGAGAGCAGAGCATGAGATTAGAGGA	2459
Qy	1211	TGAGCCGGAGCCAGAGCACACAAATGAGAGGGCTGTGACACAGCTTCCGCGCCACGGCTT	1270
Db	2460	GCAGAGAGCAGAGTTAGAGAGCAGAGACAGAGCATGAGATTAGAGAGCAGAGCAGAGATTAG	2518
Qy	1271	GAGCTCTCCGAGAGCTCTGCTTGAAGTTTGCGCGCGCGCGCGAGAGGCCAGAGGCCAAGCT	1330
Db	2519	AGGAGCAGAGAGTGAAGAGCAAGCAGAGGTTGAAAGACAAAGAGCAGAGCAGAGAG	2578
Qy	1331	TGGGAGCCCTCACTAGAGGTCGAGCTTGTGTCTGTCCCGTCAGGCCATAGCCACGCGGAGG	1390
Db	2579	AGCAGAAATTAGAGAGGTGAGAGAGCAGAGCAGAGCAGAGCAGAGAGAGAGAGAGCAGG	2638
Qy	1391	AGCTGCACGACAGCAGCGCCCGGCGCTGCAGAGAAAGAGCGCTGCGCAGCAGGTC	1450
Db	2639	AGTTAGAGAGGTGAAGAGCAGGAAGAGCAGAGTTTAGAGAGGTGGAAGACAGAGAG	2698
Qy	1451	GGAGAGCTGGGCGAAGAGCGGATGAGCTGACAGCTGCAAGTITTCATGTGTAGGCGCAGC	1510
Db	2699	AGCAGGAGTTAGAGAGGTGGAAGAGCAGAGCAGCAGAGGTTTAGAGAGGTGGAAGAGC	2758
Qy	1511	TACTGCGCTGGAAGGCGAGGCTCAGAGCGGCGCAGCAGCTGGAG	1551
Db	2759	AGGAGCAGAGGAGGTGGAACAGCAGAGAGCAGAGACGTTG	2799

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RESULT 5
US-09-410-399-1
: Sequence 1, Application US/09410399
: Patent No. 6482587
: GENERAL INFORMATION:
: APPLICANT: Robertson, Erle S.
: APPLICANT: Colter, Murray A.
: TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
: TITLE OF INVENTION: to Genomic Host DNA
: FILE REFERENCE: UM-03778
: CURRENT APPLICATION NUMBER: US/09/410,399
: CURRENT FILING DATE: 1999-10-01
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3489
: TYPE: DNA
: ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

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Query March	4.6%	Score 101;	DB 4;	Length 3489;
Best Local Similarity	44.9%;	Pred. No. 1.2e-11;		
Matches 476;	Conservative 0;	Mismatches 575;	Indels 10;	Gaps 2;
OY	491	GACTCAGCTGCTGATGACTGAGGTCATATAAGCTGAGAGAAAGGTCGACGACCTGACCG	550	

Db	1749	GCACACAGAGGGGAGCCACAGACAGGGGGAGCCACAGACAGAGATAGACAGACAGAGCA	1808
Oy	551	GCTGCTGAGCTCCAAAGATGATCTTACTCAAGAGCTGCGGTTGAAGACAGCCTGCTCG	610
Db	1809	TGAGCAGACAGAGGATGAGCAGCAGCAGGATGAGCAGCAGAGATGAGCAGCAGGAG	1868
Oy	611	CAAGCAGCAGAGGCTGTGAGAGGGCTCAAGGAGAGATGAGAGGCGCGCAGCCCGGAGCT	670
Db	1869	TGAGCAGACAGAGATGAGCAGCAGCAGGATGAGCAGCAGAGATGAGCAGCAGCAGGA	1928
Oy	671	CAAGCGCTGCAAGAGGAGAACTAACGACTGCGCATGCGCTGCGCAGCAGAGTGAAGA	730
Db	1929	TGAGCAGACAGAGATGAGCAGCAGCAGATGAGCAGCAGCAGAGATGAGCAGCAGGA	1988
Oy	731	GAAGGCGCGCGCTCATGCGAAACGGTGACTTGACGCTGAGATTGACCAAGCTCAAGCA	790
Db	1989	TGAGCAGACAGAGATGAGCAGCAGCAGGATGAGCAGCAGCAGAGATGAGCAGCAGGA	2048
Oy	791	CAGCCTTATAGAGCCAGAGACCACTGCAAGAGTGAAGCGCAACACGCTGAAGCTCAG	850
Db	2049	TGAGCAGACAGAGATGAGCAGCAGCAGATGAGCAGCAGCAGAGATGAGCAGCAGGA	2108
Oy	851	GCAAGCATGAGAGAGCGGCCACAGCCAGAGCTGCTGTGGAGAGTGCAGCAGAGAAAGGC	910
Db	2109	GGATGAGCAGAGAGCAGAGATGAGCAGAGGACAGCAGATGAGCAGCAGAGTGAAGCA	2168
Oy	911	CTTGCTTCAGAGCCCGGCTGAGAGGCTGAGGCGCTCCGTCAGAGAGGAGAACTGACAG	970
Db	2169	GCAAGCAGCAGAGATGAGCAGCAGCAGCAGATGAGCAGCAGCAGCAGAGAGATGAGCAGCAGCA	2228
Oy	971	GAGCAGCCCTTACATCCAGGTACTGAGAGAGACTGCGCGCAGGCGCTGCGGGACCA	1030
Db	2229	GCAAGATGAGCAGCAGCAGCAGAGATGAACAGAGCAGCAGAGAGGACAGAGCAGCAGGA	2288
Oy	1031	GGAAGCAGGCCAACACCACTCTTCCCTCGGCGCAGAGACTCCGCCAGGGCCAGGCCAGCG	1090
Db	2289	GGAGCAGAGCAGAGATTAGAGAGCAGAGCAGAGAGTTA-----GAGGATCCAGA	2339
Oy	1091	CCTCGGCTGATGAGAGAGAGAGATGTTGCAAGTCAAGTGCCTGCGCACTAACCTTAAGAA	1150
Db	2340	GCAAGAGTTTGAAGAGCAGAGGCTTAAAGAGACAGAGGACAGAGATTAAGAGAGCA	2399
Oy	1151	CTCCAGATGTAACAAGACCGCACTCGAGGCCATCTTGCTCAGATGAGAGAGGTCCGCA	1210
Db	2400	GGAGCAGAGATTAGAGAGCAGAGCAGAGGATTAAAGACAGAGAGCAGAGATTAAAGAGAA	2459
Oy	1211	TGAGCGGAGCCAGAGCACAATAATGAGGGGCTGTGACCAAGCTCCGCGCCAGCGGCTT	1270
Db	2460	GCAAGACAGAGATTAGAGAGCAGGAGCAGAGGATTGAGAGACAGAGACAGAGATTGAG	2518
Oy	1271	GAGCTCTCCGAGAGCCTCTGCTTGGAATTTGGGCGGCGCGGCCAGAGGGCCACAGGCCAAGCT	1330
Db	2519	AGGAGCAGAGAGTGAAGACCAAGCAGAGAGGTGGAAGCAAGACAGAGCAGAGAGAG	2578
Oy	1331	TGGGAGCCTCACTGAGGGTCCGCTTGTGCTGTCCGCTCAGGCGCATTAAGCAGCGGGAGG	1390
Db	2579	AGCAGGAATTAAGAGAGTGAAGAGCAAAAGCAGAGCAGCAGAGAGCAGAGAGAGCAGG	2638
Oy	1391	AGCTGACGCAAGCAGACGCCCGGGGCGCTGCAAGAGAAAGACGCGCTGCGCAGCAGGTC	1450
Db	2639	AGTTAGAGAGAGTTGAAGACAGAGAAAGCAGAGGATTAAAGAGAGTGAAGAGCAGGAAG	2698
Oy	1451	GGAGAGCTGGGCGAGAAAGCGGATGAGCTGCAGCTGCAGGTGTTCAATGTGAGGCGCAGC	1510
Db	2699	AGCAGAGATTAAAGAGAGTGAAGAAAGCAGAGCAGCAGAGTTTGAAGAGGTGGAAGAGC	2758
Oy	1511	TACTGAGCGTGAAGGAGCGGCTCAGGCGGACAGCAGCTGAG	1551
Db	2759	AGGAGCAGAGAGGGGTGAACAGCAGAGAGCAGAGACGATG	2799

RESULT 6
US-08-770-379-20/c

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; Sequence 20, Application US/08770379
; Patent No. 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-20

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Query Match 4.68; Score 101; DB 2; Length 32207;
Best Local Similarity 44.98; Pred. No. 1.9e-11;
Matches 476; Conservative 0; Mismatches 575; Indels 10; Gaps 2;

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QY 491 GACTCAGCTGCTGTGATGATGAGGTGATGAGAGTGCAGAGAGAGAGTGCAGAGCTGACCGC 550
DB 20248 GCCACAGCAGCGGAGGAGCCAGCAGCGGAGCCACAGCAGCAGATGAGCAGCAGCA 20189
QY 551 GCTGCTGAGCTCCAAAGATGATCTTCATCAAGAGCTGCGGCTGAGAGACAGCTGTGCG 610
DB 20188 TGAGCAGCAGAGATGATGAGCAGCAGCAGATGAGCAGCAGCAGATGAGCAGCAGCA 20129
QY 611 CAAGCAGCAGAGAGCTGTGAGAGCTTCAGAGAGAGTGCAGAGCCGCGCAGCT 670
DB 20128 TGAGCAGCAGAGATGATGAGCAGCAGCAGATGAGCAGCAGCAGATGAGCAGCAGCA 20069
QY 671 CAAGCAGCTGCAAGAGAGAGAACTACGACCTGGCCATCGGCTGCGCAGACAGAGTAGGA 730
DB 20068 TGAGCAGCAGAGATGATGAGCAGCAGCAGATGAGCAGCAGCAGCAGATGAGCAGCAGCA 20009
QY 731 GAAGGGGCGCGCTGATGCGGAGACCTGACCTGACCTGAGATTGACAGCTCAAGCA 790
DB 20008 TGAGCAGCAGAGATGATGAGCAGCAGCAGATGAGCAGCAGCAGATGAGCAGCAGCA 19949
QY 791 CAGCCTCATGAGGCGCAGAGAGCACTGCAAGGTGAGCGCAGCAGCAGCTGAAGCTCAG 850
DB 19948 TGAGCAGCAGAGATGATGAGCAGCAGCAGATGAGCAGCAGCAGATGAGCAGCAGCA 19889
QY 851 GCAGCCATGAGAGAGCGCCCGCAGCAGAGCTCTGTGGAGCTGAGCAGAGAGAGGC 910

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DB 19888 GATGAGCAGAGAGCAGAGATGAGCAGCAGCAGCAGATGAGCAGCAGCAGCAGATGAGCA 19829
QY 911 CTTGCTCCAGGCGCGGTGAGAGAGCTGAGAGCTCCCTCCAGAGAGGAGAGCTGACAG 970
DB 19828 GCAGCAGCAGAGATGAGCAGCAGCAGCAGATGAGCAGCAGCAGCAGCAGATGAGCAGCA 19769
QY 971 GAGCAGCCCTCACTCCAGAGTCTGAGAGAGAGTGGCGGCAAGCGCTGGCGGAGCCACCA 1030
DB 19768 GCAGATGAGCAGCAGCAGAGATGAGCAGCAGCAGCAGCAGAGAGAGAGAGCAGCAGCA 19709
QY 1031 GAGCAGGCGCAACCACTCTTCTCCCTGCGCAAGAGCCTCCGCCAGGCGAGCGCCACAG 1090
DB 19708 GAGCAGAGCAGCAGATGAGAGAGCAGCAGCAGAGATTA-----GAGATTCAGCA 19658
QY 1091 CTTCCGCTGATGAGAGAGAGAGATGTTGAGAGTTCAGAGTTCCTGCACTAGCTAAGGA 1150
DB 19657 GCAGAGTTAGAGAGCAGCAGCAGAGATTAAGAGCAGCAGAGCAGAGATTAAGAGAGCA 19598
QY 1151 CTCCAGATGTAACAAGACCGCATGAGGCCATCTCTGCTGCAATGAGAGAGTCCCAT 1210
DB 19597 GAGCAGAGAGATTAAGAGAGCAGCAGCAGAGATTAAGAGAGCAGAGAGAGATTAAGGA 19538
QY 1211 TGAGCGGAGCAGAGCAGCAGCAAAATGAGAGGCTGTGACAGCTCCGCGCCAGCGGCTT 1270
DB 19537 GCAGAGCAGAGATTAAGAGAGCAGCAGCAGAGATTA-GAGAGCAGAGAGAGAGATTAAG 19479
QY 1271 GACGTCTCCGAGAGCTCTGCTGTAAGTTGAGGCGGCGGCGGAGGCGCAAGCT 1330
DB 19478 AGAGCAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19419
QY 1331 TGAGGCGCTCACTAGAGAGTCCGCTTGTGCTGCTCCGCTCAGGCCATAGCCACGCGGAGG 1390
DB 19418 AGCAGATTAAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 19359
QY 1391 AGCTGACGACAGCAGCAGCAGCGCGGCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGTGC 1450
DB 19358 AGTTAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19299
QY 1451 GAGAGCTGGCGAGAGAGCGGATGAGCTGACAGCTGCAAGTGTTCAGAGTGAAGCGCAGC 1510
DB 19298 AGCAGAGATTAAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGATTAAGAGAGTGAAGAGC 19239
QY 1511 TACTGCGCGTGAGAGGAGCGCTCAGAGCGCAGCAGCTGAG 1551
DB 19238 AGAGCAGCAGAGGAGGTGAACAAGCAGCAGCAGAGAGAGCTG 19198

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RESULT 7
US-08-757-669A-20/C
; Sequence 20, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; TITLE OF INVENTION: UNIQUS ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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[illegible]

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RESULT 9
US-09-249-585A-2
Sequence 2, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1926)
OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

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Query Match	4.6%;	Score 100.6;	DB 4;	Length 1926;
Best Local Similarity	48.5%;	Pred. No. 1.3e-11;		
Matches 277; Conservative	0;	Mismatches 294;	Indels 0;	Gaps 0;

QY	468	GAACGCGCTCCGGAGAGTCAAGCGCTTGACTCAACTCTCTATATCTGAGGTCATGTAAGCTGCAAG	527
Db	356	GAGGGGCAAGAGGGGCAAGAGCAAGAGAGAGGGCAAGAGCAAGAGGAGGGGCAAGAGGGG	415
QY	528	AAGAAAGTTCAGAGACTTGACCCGCTTGAGCTCCAAAGATGACTTCATCAAGAGAGCTG	587
Db	416	CAGAGAGGGGCAAGAGCAAGAGAGAGGGGCAAGAACAGAGAGGAGGAGAGAGGGGCAAGAG	475
QY	588	CGGAGTGAAGGACAAAGCTTGCTGCGCAAGACCAAGAGCGTGTGCAGAGGCTCAAGAGAGAG	647
Db	476	CAGAGAGAGGGGCAAGAGAGGGGCAAGAGAGGGGCAAGAACAGAGAGGAGGCGCAGAGAGCAGAG	535
QY	648	TTCGAGAGCCGGACAGCCCGAGCTTCAGAGCGCTGCAGAGAGAGAACTTACGACTTGCCATG	707
Db	536	GAGGGGCAAGAGGGGGCAAGAGACAGAGAGAGGGGCAAGAGGGGCAAGAGGGGCAAGAGGAG	595
QY	708	CGCCTGCGGCACCAAGAGTGAAGAGAGAGGGGCGCCGCTCATGCGGAACCGTGACTGCGAG	767
Db	596	GAGGAGGGGCAAGAGCAAGAGAGGGGCAAGAGGGGCAAGAGGGGCAAGAGCAAGAGAGGGGAG	655
QY	768	CTGAGAGATTGACCAAGCTTCAGACCAAGCTCTATGAAGCCGAGGACGACTGCAAGGTGGAG	827
Db	656	GAGCAAGAGAGGGGCAAGAGAGGGGCAAGAGAGGGGCAAGAGAGGAGAGGAGGAGCAAGAGCAGAG	715
QY	828	CGCAAGGACACGCTGGAAGCTCAGGCAAGCCATGGAAGAGAGGCCCAAGAGAGCTGCTG	887
Db	716	GGGCAAGAGCAAGAGGGGCAAGACCAAGAGAGGGGCAAGAGAGGGGCAAGAGCAAGAGAGGGGCAAG	775
QY	888	TTCGAGCTGCAAGCAAGAGAAAGCCCTGCTCAAGGCCCGAGGTGCAGAGAGCTGAGAGGCTCC	947
Db	776	GAGGGGCAAGAGCAAGAGAGGGGCAAGAGAGGGGCAAGAGCAGAGAGAGGGGCAAGAGGGGCAAG	835
QY	948	GATCAGAGAGGGAGAGCTGGAACAGAGAGAGCCCTTACATCCAGAGTACTGAGAGAGAGCTGG	1007
Db	836	GAGCAAGAGAGGGGCAAGAGAGGGGCAAGAGCAAGAGAGGGGCAAGAGAGGGGCAAGAGCAGAG	895
QY	1008	CGGCAAGGCGCTGCGGGAACCAAGAGAGCAGG	1038
Db	896	GGGCAAGAGAGGGGCAAGAGCAAGAGAGGGGCAAG	926

RESULT 10
US-09-410-399-3
Sequence 3. Application US/09410399

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/ APPLICANT: Robertson, Etile S.
/ APPLICANT: Cotter, Murray A.
/ TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
/ TITLE OF INVENTION: to Genomic Host DNA
/ FILE REFERENCE: UM-03778
/ CURRENT APPLICATION NUMBER: US/09/410.399
/ CURRENT FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver, 2.0
/ SEQ ID NO 3
/ LENGTH: 1926
/ TYPE: DNA
/ ORGANISM: Epstein-Barr virus
/ US-09-410-399-3

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Query Match	4.6%	Score 100.6	DB 4	Length 1926
Best Local Similarity	48.5%	Pred. No. 1.3e-11		
Matches 277	Conservative 0	Mismatches 294	Indels 0	Gaps 0
QY	468	GACGGCTCCGGGAGTCAAGGCTTCACTCACTGTGATACAGTCAATGAAGCTGACG	527	
DQ	356	GAGGGCCAGAGACGGGCGAGACAGAGAGAGGGCGTACGAGGAGGAGAGGGCGCCAGAGGGG	415	

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-050-863-2

Query Match      4.6%; Score 100.6; DB 3; Length 2580;
Best Local Similarity 48.5%; Pred. No. 1,46-11;
Matches 277; Conservative 0; Mismatches 294; Indels 0; Gaps 0;

QY 528 AAGAAGTCAAGACCTGACCGCTGTGAGCTCCAAAGATGACTTTCATCAAGAGCTG 587
DB 416 CAGAGAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
QY 588 CGGGTGAAGACAAGCTGTGTGCGCAAGACAAGAGACCTGTGTCAAGAGCTCAAGAGAGAG 647
DB 476 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535
QY 648 TGCAGAGCCGCGCAGCCGAGCTCAAGCCGTGCAAGAGAGAGAACTACCACTTGGCATG 707
DB 536 GAGGGGCAAGAGAGGCGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
QY 708 CGCTTGGCCCAACCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 767
DB 596 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
QY 768 CTGAGATTGACCAAGCTCAAGACAAGCTCTATGAAGCCGAGGACGACTGCAAGGTGAG 827
DB 656 GAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 715
QY 828 CGCAAGACAAGCTGAAGCTCAGGCAAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 887
DB 716 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 775
QY 888 TGGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
DB 776 GAGGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 835
QY 948 GTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1007
DB 836 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895
QY 1008 CGGCAAGCGCTGCGGAGCCACCAAGAGAGAGAG 1038
DB 896 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926

RESULT 11
US-09-050-863-2
; Sequence 2, Application US/09050863
; Patent No. 6114111
; GENERAL INFORMATION:
; APPLICANT: Lao, Yang
; APPLICANT: Hiang, Betty
; APPLICANT: Payan, Don
; TITLE OF INVENTION: Mammalian Protein Interaction Cloning
; TITLE OF INVENTION: System
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albrighton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/050, 863
; FILING DATE: 30-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-65638/DBE/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-050-863-2

Query Match      4.6%; Score 100.6; DB 3; Length 2580;
Best Local Similarity 48.5%; Pred. No. 1,46-11;
Matches 277; Conservative 0; Mismatches 294; Indels 0; Gaps 0;

QY 468 GAGCGGTCCGGGAGGTAGAGGCTGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 527
DB 739 GAGGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
QY 528 AAGAAGTCAAGACCTGACCGCTGTGAGCTCCAAAGTGAAGTTCATCAAGAGAGAGAG 587
DB 799 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
QY 588 CGGGTGAAGACAAGCTGTGTGCGCAAGACAAGAGACCTGTGTCAAGAGCTCAAGAGAGAG 647
DB 859 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
QY 648 TGCAGAGCCGCGCAGCCGAGCTCAAGCCGTGCAAGAGAGAGAACTACCACTTGGCATG 707
DB 919 GAGGGGCAAGAGAGGCGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
QY 708 CGCTTGGCCCAACCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 767
DB 979 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
QY 768 CTGAGATTGACCAAGCTCAAGACAAGCTCTATGAAGCCGAGGACGACTGCAAGGTGAG 827
DB 1039 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
QY 828 CGCAAGACAAGCTGAAGCTCAGGCAAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 887
DB 1099 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
QY 888 TGGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
DB 1159 GAGGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
QY 948 GTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1007
DB 1219 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
QY 1008 CGGCAAGCGCTGCGGAGCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
DB 1279 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1309

RESULT 12
US-09-359-081-2
; Sequence 2, Application US/09359081
; Patent No. 6316223
; GENERAL INFORMATION:
; APPLICANT: Lao, Yang
; APPLICANT: Hiang, Betty
; APPLICANT: Payan, Don
; TITLE OF INVENTION: Mammalian Protein Interaction Cloning
; TITLE OF INVENTION: System
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albrighton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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Tue Feb 24 09:52:04 2004

us-10-032-159a-19.rni

Page 12

Search completed: February 23, 2004, 13:33:16
Job time : 151 secs

QY 121 AGACCTCAGCCTGCTGTGAGGCAATGTGGCACTAGAGAAAGATGACGAGTGTGGA 180
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Db 181 AGCTCTGAGAGGCTTCCGGGTGACGCTCACTCGGTCATCGACCCCTCAGCATCAC 240
QY 241 CTTACCTGCGGAGTGCAGAGGTCCTGAACTTGAATGAGAGAGAGTGTCTCAGCAAC 300
Db 241 CTTACCTGCGGAGTGCAGAGGTCCTGAACTTGAATGAGAGAGAGTGTCTCAGCAAC 300
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Db 301 CCAACTGTGTCACTCCGCAACGAAAGTGTGTCTCTGCAATCTCTGACGCGGACCG 360
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Db 361 GGCACAGAGGCTACGAGGCTTCTCTGAGAGGCTTACTACCGGAGCTGTACA 420
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Db 421 AGAAGCTCAGGCAAGAGAGGCGCGGCTTCTCCATGATCACTGACGCGTCCGGG 480
QY 481 AGTCAGGCTGACTAGCTGTGTATGATCTGAGGTCACTGAACTGCAAGAAAGTGTGAG 540
Db 481 AGTCAGGCTGACTAGCTGTGTATGATCTGAGGTCACTGAACTGCAAGAAAGTGTGAG 540
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Db 541 ACCTGACCGGCTGTGTGAGTCTCAAGATGATCTTCACTGAGAGGCTGCGGGTGAAGACA 600
QY 601 GCGTGTGCGCAAGCAAGAGGCGTGTGAGAGGCTCAAGAGAGGCTGCGAGCGGCA 660
Db 601 GCGTGTGCGCAAGCAAGAGGCGTGTGAGAGGCTCAAGAGAGGCTGCGAGCGGCA 660
QY 661 GCGGAGCTCAGAGGCTGCAAGAGAGAGAACTAGACCTGACCTGCGCTGCGGCAAC 720
Db 661 GCGGAGCTCAGAGGCTGCAAGAGAGAGAACTAGACCTGACCTGCGCTGCGGCAAC 720
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Db 721 AGAGTGAAGAAAGGCGCGGCTCATGCGAAACCTGACCTGACGCTTGAATGACC 780
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Db 781 AGCTCAAGCAAGGCTTCAATGAAAGGCGAGAGCACTGCAAGGCTGAGCCCAAGCACCC 840
QY 841 TGAAGCTCAGGCAAGGCTGAGAGAGGCGGCAAGAGGCTGAGAGGCTGAGAGG 900
Db 841 TGAAGCTCAGGCAAGGCTGAGAGAGGCGGCAAGAGGCTGAGAGGCTGAGAGG 900
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QY 1141 TAGGTAAAGACTCAAGATGTACAGAGAGCGCATCGAGGCTGCTGCAAGTGAAG 1200
Db 1141 TAGGTAAAGACTCAAGATGTACAGAGAGCGCATCGAGGCTGCTGCAAGTGAAG 1200
QY 1201 AGGTGCGCATTTAGCGGAGCAAGAGCACAAAATGAGAGGCGCTGTGACCAAGCTCCGCGC 1260

Db 1201 AGGTGCGCATTTAGCGGAGCAAGAGCACAAAATGAGAGGCGCTGTGACCAAGCTCCGCGC 1260
QY 1261 CCAAGGCTTGAAGCTTCTCCGAGGCTTGTGAGTGTGAGGCGGCGGCGGCGGCGG 1320
Db 1261 CCAAGGCTTGAAGCTTCTCCGAGGCTTGTGAGTGTGAGGCGGCGGCGGCGGCGG 1320
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Db 1321 AGGCAAGCTTGGGAGGCTTCACTGAGAGGCTTGTGCTGTCTCCGTCAGAGCTATAGC 1380
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Db 1501 GAGGCGAGCTACTGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 CTGAGCTCCGACCTGGAAGAGTGTCTACCAAGAGAGTCCAGAGAGCTTCACTCCCGAG 1620
Db 1561 CTGAGCTCCGACCTGGAAGAGTGTCTACCAAGAGAGTCCAGAGAGCTTCACTCCCGAG 1620
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Db 1621 GACCTGAGAGCAACCAAGCTCTCAGACAAAGGCTGCTCCGCGGAGGAGAGAGAG 1680
QY 1681 CAGGCTTGTGAGCTGTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 CAGGCTTGTGAGCTGTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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QY 1861 GAGAAACACAG 1920
Db 1861 GAGAAACACAG 1920
QY 1921 CCGAGCGCTGCTGACTGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
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QY 1981 ACTGCGGAG 2040
Db 1981 ACTGCGGAG 2040
QY 2041 CTACAG 2100
Db 2041 CTACAG 2100
QY 2101 TAAACAGAAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
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QY 2161 AGCAGGAGTGAACCGCG 2176
Db 2161 AGCAGGAGTGAACCGCG 2176

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1  APPLICANT: Berlin, John
2  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
3  TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
4  FILE REFERENCE: 07334-327001
5  CURRENT APPLICATION NUMBER: US/09/798,412
6  CURRENT FILING DATE: 2001-03-02
7  PRIOR APPLICATION NUMBER: US 09/728,260
8  PRIOR FILING DATE: 2000-12-01
9  PRIOR APPLICATION NUMBER: US 09/685,791
10 PRIOR FILING DATE: 2000-10-10
11 PRIOR APPLICATION NUMBER: US 09/513,904
12 PRIOR FILING DATE: 2000-02-25
13 PRIOR APPLICATION NUMBER: US 09/507,533
14 PRIOR FILING DATE: 2000-02-18
15 PRIOR APPLICATION NUMBER: US 60/168,780
16 PRIOR FILING DATE: 1999-12-03
17 NUMBER OF SEQ ID NOS: 19
18 SOFTWARE: FASTSEQ for Windows Version 4.0
19 SEQ ID NO 4
20 LENGTH: 2098
21 TYPE: DNA
22 ORGANISM: Homo sapiens
23 FEATURE:
24 NAME/KEY: CDS
25 LOCATION: (144)...(1751)
26 US-09-798-412-4

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Query Match	80.2%	Score 1746;	DB 11,	Length 2098;
Best Local Similarity	89.9%;	Pred. No. 0;		
Matches 199;	Conservative	0;	Mismatches 5;	Indels 220;
				Gaps 3;

OY	25	CGGGTGTCTCCCTCCCTCCCTGAGCCCGGAGAGATATCCACAGAGGCTCCGCGGCTCAG	84
Db	22	GTCTCGGCTCTCTCTCCCTCCCTGAGCCCGGAGAGATATCCACAGAGGCTCCGCGGCTCAG	81
OY	85	GCTCTGTGTGTCTGCAGTGAGGTGACTCTTGAGAACCTTCAGCTGCTGTGTAG	144
Db	82	GCTCTGTGTGTCTGCAGTGAGGTGACTCTTGAGAACCTTCAGCTGCTGTGTAG	141
OY	145	CCATGTCCGAACTTACGAGAACGATGACGAGTCTGGAACGTCTTGAGGGGCTTCCGGGTGA	204
Db	142	CCATGTCCGAACTTACGAGAACGATGACGAGTCTGGAACGTCTTGAGGGGCTTCCGGGTGA	201
OY	205	CGCTACCTCCGGTCAATCAGACCCCTACACCATACACCTTACCTGGGAGATGCAAGTCC	264
Db	202	CGCTACCTCCGGTCAATCAGACCCCTACAGCATACACCTTACCTGGGAGATGCAAGTCC	261
OY	265	TGAACCTTGATGATGAGGACGAGGTGCTCAGACGCCCACTCTGTATCCGCAACCGA	324
Db	262	TGAACCTTGATGATGAGGACGAGGTGCTCAGACGCCCACTCTGTATCCGCAACCGA	321
OY	325	AAGTGGGTGTCTCTGTGACATCTCTGCAGCGGACCGGCAACAAGGGCTACGTGGCTTCC	384
Db	322	AAGTGGGTGTCTCTGTGACATCTCTGCAGCGGACCGGCAACAAGGGCTACGTGGCTTCC	381
OY	385	TCGAGAGCTTGAGGCTTACTTACCCTGACTGTATCAAGAGTCAACAGGCAAGGACCGG	444
Db	382	TCGAGAGCTTGAGGCTTACTTACCCTGACTGTATCAAGAGTCAACAGGCAAGGACCGG	441
OY	445	CCCGGCTTTCTCCATGATCATCGACGAGTCCGGGGAGTCAAGGCTTGACTGAGCTGTGA	504
Db	442	CCCGGCTTTCTCCATGATCATCGACGAGTCCGGGGAGTCAAGGCTTGACTGAGCTGTGA	501
OY	505	TGACTGAGCTCATGAGCTGCGAAGAAAGTGCAGAGACTTGCACGGCTGTGAGCTTCA	564
Db	502	TGACTGAGCTCATGAGCTGCGAAGAAAGTGCAGAGACTTGCACGGCTGTGAGCTTCA	561
OY	565	AAGATGACTTTCATCAAGAGCTGCGGGGTGAAGGACAGCTGTGTGGCAAGACCCAGAGGC	624
Db	562	AAGATGACTTTCATCAAGAGCTGCGGGGTGAAGGACAGCTGTGTGGCAAGACCCAGAGGC	621
OY	625	GTGTGCAGAGGCTCAAGAGGAGTGTGCGAGCCCGGAGGCTCGAGGCTCAAGGCTTCAAGG	684

Db	622	GTGTGCAAGAGGCTCAAGAGAGATGTCCAGAGCCGGGCAAGCCGCGAGTCTCAAGGCTGCAAGG	681
OY	685	AGAGAACTACAGACTTGCCCATGCGCCTTGCGCAACAGATGAGAGAGAGAGCGCCGCGC	744
Db	682	AGGAACTACGACTTGCCCATGCGCCTTGCGCAACAGATGAGAGAGAGAGCGCCGCGC	741
OY	745	TCATGCGGAACCGTGACTTGCACTGGAAGATTGACCACTCAAGCACAGCTCATGAAG	804
Db	742	TCATGCGGAACCGTGACTTGCACTGGAAGATTGACCACTCAAGCACAGCTCATGAAG	801
OY	805	CCGAGGAGACTGCAAGGTGGAAGGCAAGCACAGCTGAAGCTCAAGGCAAGCCATGAGC	864
Db	802	CCGAGGAGACTGCAAGGTGGAAGGCAAGCACAGCTGAAGCTCAAGGCAAGCCATGAGC	861
OY	865	AGCGGCCAGCCAGAGAGTGTGTGTGAGAGCTGCAAGCAAGAGAGAGCCCTGTCCAGGCC	924
Db	862	AGCGGCCAGCCAGAGAGTGTGTGTGAGAGCTGCAAGCAAGAGAGAGCCCTGTCCAGGCC	921
OY	925	GGGTGCAAGAGACTGGAAGGCTTCGCTCCAGAGGGGAGCTGGAACAGAGCAAGCCCTACA	984
Db	922	GGGTGCAAGAGACTGGAAGGCTTCGCTCCAGAGGGGAGCTGGAACAGAGCAAGCCCTACA	981
OY	985	TCGAGGATCTGGAAGAGACTGCGCGAGAGGGCTGCGGGAACACAGAGAGAGGCGCAAC	1044
Db	982	TCGAGGATCTGGAAGAGACTGCGCGAGAGGGCTGCGGGAACACAGAGAGAGGCGCAAC	1041
OY	1045	CCATCTTCTCCCTGCGCAAGGACTCGGCACAGGCGAGAGGCCGACAGCCCTCCGATGATG	1104
Db	1042	CCATCTTCTCCCTGCGCAAGGACTCGGCACAGGCGAGAGGCCGACAGCCCTCCGATGATG	1101
OY	1105	AGAGAGAGAGATGTTGAGCTGCAAGTGCCTGAGCACTACGTAAAGACTCCAAATGTACA	1164
Db	1102	AGAGAGAGAGATGTTGAGCTGCAAGTGCCTGAGCACTACGTAAAGACTCCAAATGTACA	1161
OY	1165	AGAGACCGATGGAAGCCCATCTGCTGCAAGATGAGAGAGAGTGCCTATGAGCGGACCAAG	1224
Db	1162	AGAGACCGATGGAAGCCCATCTGCTGCAAGATGAGAGAGAGTGCCTATGAGCGGACCAAG	1221
OY	1225	GCAACAATGAGAGGGCTGTGACCAAGCTCCGCGCCAGAGGGCTTGAACGTCTCCGAG	1284
Db	1218	-----	1217
OY	1285	CCTCTGTTGAGATTGGGCGGCGCGGCGAGAGGCCAGAGGCGAAGCTTGGGGCCTCACTG	1344
Db	1218	-----	1217
OY	1345	AGGCTCGGCTTGTGTGTCTCCGTCAGGCCATAGCCACGCGGAGAGAGCTGACAGCAC	1404
Db	1218	-----	1217
OY	1405	CACGCCCGGGGCTGCAAG	1464
Db	1254	CACGCCCGGGGCTGCAAG	1313
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Db	1314	AAGGCGAGTGAAGCTGCAAGCTGCAAGTGTTCAGATGTGAGGCGGCACTTACTGCGGTGAG	1373
OY	1525	GCGAGGCTCAGAGGCGGCAAGAGCTGGAAGACGCTGCTCTGAGCTTCGACTTGGAAGATGC	1584
Db	1374	GCGAGGCTCAGAGGCGGCAAGAGCTGGAAGACGCTGCTCTGAGCTTCGACTTGGAAGATGC	1433
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Db	1434	TCACCCAGAGAGTCCAGAGAGCTTCACCTCCCGAGAGCTGGAAGAGAGAGAGAGAGAGAG	1493
OY	1645	GACAAAGGCTGCTGTCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1704
Db	1494	GACAAAGGCTGCTGTCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1553
OY	1705	GAGCAGGTTTGGCGAACCCTCATGACGACAGCTTGACAGCGGAGAGCGCCCGAGAG	1764
Db	1554	GAGCAGGTTTGGCGAACCCTCATGACGACAGCTTGACAGCGGAGAGCGCCCGAGAG	1613

QY	1765	JAGCGGCGCGCCCTCAAGAGAGGTTTGAAGACTACCGCAGAGAGCGGCCCTCAGGAG	1824
Db	1614	GAGCGCGCGCGCCCTCAAGAGAGGTTTGAAGACTACCGCAGAGAGCGGCCCTCAGGAG	1673
QY	1825	ATGCAGAAAGATGGCGGACAGGAGAGAGACCAGGAGAACACCAACCGGACGCAAC	1884
Db	1674	ATGCAGAAAGATGGCGGACAGGAGAGAGACCAGGAGAACACCAACCGGACGCAAC	1733
QY	1885	ACCGACTGAGGGCTCTAGCCGCA-----	1910
Db	1734	ACCGACTGAGGGCTCTAGCCGACAGCGACAGGCCCCGACAGGACACCCACCGG	1753
QY	1911	-----GCAACTTCCCCGAGCCGTGCT	1933
Db	1794	CCCGGCTGCACCCGCGGATGCCAGCCCTGGGACCAAGCTTCCCGAGCGTGCT	1853
QY	1994	GACTTGGCTGGAAACGAGAAATCTGTGTCCTGAAAGGCGGACGCTCGCGGCAAT	1993
Db	1864	GACTTGGCTGGAAACGAGAAATCTGTGTCCTGAAAGGCGGACGCTCGCGGCAAT	1913
QY	1994	GGGGCGGTTGTTAAGCGGCACTATTTGGGAGGCGCATCGGCTGCTACCAACCCCA	2053
Db	1914	GGGCGCGTTGTTAAGCGGCACTATTTGGGAGGCGCATCGGCTGCTACCAACCCCA	1973
QY	2054	TGCACAGCCACTGTGTGTAACCTTCAGATCTGTCTGTTACCATGTAAACACAAATAC	2113
Db	1974	TGCACAGCCACTGTGTGTAACCTTCAGATCTGTCTGTTACCATGTAAACACAAATAC	2033
QY	2114	ATGCATGATGTGTATTAGTGT-TAGAAACACAGCTGCTAATTAACAGACGGGTAC	2172
Db	2034	ATGCATGATGTGTATTAGTGTAAAGAAACACAGCTGCTAATTAACAGACGGGTAC	2093
QY	2176	CCGC 2176	
Db	2094	CCGC 2097	
RESULT 3			
US-10-325-917-4			
; Sequence 4, Application US/10325917			
; Publication No. US20030113787A1			
; GENERAL INFORMATION:			
; APPLICANT: Bertin, John			
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF			
; FILE REFERENCE: 07334-327001			
; CURRENT FILING DATE: 2002-12-20			
; PRIOR APPLICATION NUMBER: US/09/798,412			
; PRIOR FILING DATE: 2001-03-02			
; PRIOR APPLICATION NUMBER: US 09/728,260			
; PRIOR FILING DATE: 2000-12-01			
; PRIOR APPLICATION NUMBER: US 09/685,791			
; PRIOR FILING DATE: 2000-10-10			
; PRIOR APPLICATION NUMBER: US 09/513,904			
; PRIOR FILING DATE: 2000-02-25			
; PRIOR APPLICATION NUMBER: US 09/507,533			
; PRIOR FILING DATE: 2000-02-18			
; PRIOR APPLICATION NUMBER: US 60/168,780			
; PRIOR FILING DATE: 1999-12-03			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO: 4			
; LENGTH: 2098			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (144)...(1751)			
US-10-325-917-4			
Query Match 80.2%; Score 1746; DB 15; Length 2098;			

[illegible]

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DB 1102 AGAAGAAAGAGATGTTCCAGCTGCAAGTGCCTGCACTACGTAAAGACTCCAAATGTACA 1161
QY 1165 AGAAGCCGATCGAGGCGCATCTCTGCTGCAAGTGAAGAGAGTCCGCTTGAAGGGAACCA 1224
DB 1162 AGAAGCCGATCGAGGCGCATCTCTGCTGCAAGTGAAGAGAGTCCGCTTGAAGGGAACCA 1217
QY 1225 GCACAATAATGAGGGGCTGTGACAGGCTCCGCGCCAGGCGTTGACGTCTCCGAG 1284
DB 1218 ----- 1217
QY 1285 CCTCTGTTGAGTTGGCGCGCGGCGCCAGAGGCCCAAGCTTGAGGCTCTCACTG 1344
DB 1218 ----- 1217
QY 1345 AGGCTGGCTTGTGTCTGCTCCGCTCAGGCGCATAGCCACGCGGAGAGAGCTGCAAGCAG 1404
DB 1218 -----CAGGCGATAGCCACGCGGAGAGAGCTGCAAGCAG 1253
QY 1405 CAGCGCCGGGCGCTGCAAGAGAGAGAGCGGCTGCGCAAGAGAGTCCGGAAGCTGGCGAG 1464
DB 1254 CAGCGCCGGGCGCTGCAAGAGAGAGAGCGGCTGCGCAAGAGAGTCCGGAAGCTGGCGAG 1313
QY 1465 AAGGCGGATGAGCTGAGCTGAGAGGTTCAGTGTGAGGCGACACTGCTGGCGGTGAG 1524
DB 1314 AAGGCGGATGAGCTGAGCTGAGAGGTTCAGTGTGAGGCGACACTGCTGGCGGTGAG 1373
QY 1525 GGCAGGCTCAGGCGGCGCAGAGCTGAGAGAGCTGCTGAGTCCGACCTTGGAAGATGAG 1584
DB 1374 GGCAGGCTCAGGCGGCGCAGAGAGCTGAGAGAGCTGCTGAGTCCGACCTTGGAAGATGAG 1433
QY 1585 TCACCCAGAGAGTCCGAGAGGCTTCACTCCCGCAAGACTGAGAGACAACCAAGCTTCA 1644
DB 1434 TCACCCAGAGAGTCCGAGAGGCTTCACTCCCGCAAGACTGAGAGACAACCAAGCTTCA 1493
QY 1645 GACAAAGGCTGCTTCCGCGCGGAGAGAGCCGAAACAGAGCTTTGCAAGTCTGACCAAG 1704
DB 1494 GACAAAGGCTGCTTCCGCGCGGAGAGAGCCGAAACAGAGCTTTGCAAGTCTGACCAAG 1553
QY 1705 GAGCAGGTTTGGGGAACCCCATGACGAGGCTGAGCAGGAGGAGGCGCGCGAGAG 1764
DB 1554 GAGCAGGTTTGGGGAACCCCATGACGAGGCTGAGCAGGAGGAGGCGCGCGAGAG 1613
QY 1765 GAGCAGGCGGCGCTCAAGAGAGTGTGAGAACTACCGCAGAGAGCGGCTCTCAGAGAG 1824
DB 1614 GAGCAGGCGGCGCTCAAGAGAGTGTGAGAACTACCGCAGAGAGCGGCTCTCAGAGAG 1673
QY 1825 ATGCAAAAGAGATGCGGCGAGGAGAGAGAGCAGGAGAGACCAAGCGGAGCGAGCAAC 1884
DB 1674 ATGCAAAAGAGATGCGGCGAGGAGAGAGAGCAGGAGAGACCAAGCGGAGCGAGCAAC 1733
QY 1885 ACCGAGACTGAGGAGCTCTAGCCGCA----- 1910
DB 1734 ACCGAGACTGAGGAGCTCTAGCCGAGCAGCAGCGAGCCCGACCAAGGAGCAACCAAGCGG 1793
QY 1911 -----GCAAGCTTCCCGAGAGCGGTGCT 1933
DB 1794 CCGGAGCTGCGCAAGCGGAGGCTCCAGCGGCTGCGGCGAGAGCTTCCCGAGAGCGGTGCT 1853
QY 1934 GACTTGGCTTGAAGCAGAGATCTGTGCTGCTGAAAGGCCAGCGGAGCTGCGGAGCAAT 1993
DB 1854 GACTTGGCTTGAAGCAGAGATCTGTGCTGCTGAAAGGCCAGCGGAGCTGCGGAGCAAT 1913
QY 1994 GGGGCGGTTTGTAAAGCGGAGCTCAATTTTGGGAGGCGCAAGCGGAGCTCACCAACCCCA 2053
DB 1914 GGGGCGGTTTGTAAAGCGGAGCTCAATTTTGGGAGGCGCAAGCGGAGCTCACCAACCCCA 1973
QY 2054 TGCACACGCGCATCTGTGTAACTTCAAGAGCTGTCTTCTTCAACATGTAAACAACAATAC 2113
DB 1974 TGCACACGCGCATCTGTGTAACTTCAAGAGCTGTCTTCTTCAACATGTAAACAACAATAC 2033

QY 2114 ATGATGCACTTGTATTAGTGT--AGAAAACAGCTGCGCTAAATTAACAGCAGGGGTGAC 2172
DB 2034 ATGATGCACTGATTAAGTGTAAAGAAAACAGCTGCGCTAAATTAACAGCAGGGGTGAC 2093
QY 2173 CCGC 2176
DB 2094 CCGC 2097

RESULT 4
US-09-798-412-6
; Sequence 6, Application US/09798412
; Publication No. US20030109428A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 0734-327001
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-798-412-6

Query Match 66.6%; Score 1448.4; DB 11; Length 1608;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1607; Conservative 0; Mismatches 1; Indels 148; Gaps 1;

QY 147 ATGTCGACATACAGAAACGATAGAGAGTCTGAGAACTCTCGAGAGGCTTCCGGGTGACG 206
DB 1 ATGTCGACATACAGAAACGATAGAGAGTCTGAGAACTCTCGAGAGGCTTCCGGGTGACG 60
QY 207 CTGACCTCGGTCATGAGCCCTTCAAGCATCAACCTTAAGCTGCGGAGTGAAGTCTG 266
DB 61 CTGACCTCGGTCATGAGCCCTTCAAGCATCAACCTTAAGCTGCGGAGTGAAGTCTG 120
QY 267 AACCTGATGATGAGAGAGAGTCTCAGGAGCCCAACCTGATCATCCGAAACGAAA 326
DB 121 AACCTGATGATGAGAGAGAGTCTCAGGAGCCCAACCTGATCATCCGAAACGAAA 180
QY 327 GTGGGTGCTCTGAGCATCTTGCAGCGGAGCCGCAAAAGGCTTACGTGCTCTC 386
DB 181 GTGGGTGCTCTGAGCATCTTGCAGCGGAGCCGCAAAAGGCTTACGTGCTCTC 240
QY 387 GAGAGCTGAGAGCTCTACCCGAGCTGTACAAAGAGTCAAGGCAAGAGAGCGGCGC 446
DB 241 GAGAGCTGAGAGCTCTACCCGAGCTGTACAAAGAGTCAAGGCAAGAGAGCGGCGC 300
QY 447 CGCGCTTCTCATGATCATGAGCGCTCCGGGAGTCAAGGCTGATCAGCTGATG 506
DB 301 CGCGCTTCTCATGATCATGAGCGCTCCGGGAGTCAAGGCTGATCAGCTGATG 360
QY 507 ACTAGGTCATGAGAGCTGCAAGAGAGTGAAGAGCTGACCGGCTGCTAGCTCCAAA 566
DB 361 ACTAGGTCATGAGAGCTGCAAGAGAGTGAAGAGCTGACCGGCTGCTAGCTCCAAA 420
QY 567 GATGACTTCAAGAGAGCTGCGGAGTGAAGAGAGCTGCTGCGCAAGCAGAGAGCT 626

QY 367 GAGAGCTGAGCTCTACTACCCGAGCTGTACAGAAAGTCAAGAGGAAAGAGCCGACC 446
Db 241 GAGAGCTGAGCTCTACTACCCGAGCTGTACAGAAAGTCAAGAGGAAAGAGCCGACC 300
QY 447 GCGGCTTCTCATGATCATGACGCGCTCCGGGAGTCAAGGCTCACTCACTGCTGATG 506
Db 301 GCGGCTTCTCATGATCATGACGCGCTCCGGGAGTCAAGGCTCACTCACTGCTGATG 360
QY 507 ACTGAGGTCAAGAGCTGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 566
Db 361 ACTGAGGTCAAGAGCTGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 420
QY 567 GATGACTCATCAAGAGAGTCAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 626
Db 421 GATGACTCATCAAGAGAGTCAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 480
QY 627 GTGCAAGAGCTCAAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 686
Db 481 GTGCAAGAGCTCAAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 540
QY 687 GAGAACTACAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 746
Db 541 GAGAACTACAGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 600
QY 747 ATGCGGAAACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 806
Db 601 ATGCGGAAACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 660
QY 807 GAGGACGACTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 866
Db 661 GAGGACGACTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 720
QY 867 CGGCTCAAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 926
Db 721 CGGCTCAAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 780
QY 927 GTGCAAGAGCTGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 986
Db 781 GTGCAAGAGCTGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 840
QY 987 CAGGTACTGAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1046
Db 841 CAGGTACTGAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 900
QY 1047 ATCTTCTCCCTGAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1106
Db 901 ATCTTCTCCCTGAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 960
QY 1107 GAGAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1166
Db 961 GAGAGAGAGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1020
QY 1167 GAGCGCATGAGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1226
Db 1021 GAGCGCATGAGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1227 AACAAATGAGAGGCTGTGA 1247
Db 1081 AACAAATGAGAGGCTGTGA 1101

RESULT 7

US-09-798-412-1
; Sequence 1, Application US/09798412
; Publication No. US20030109428A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-327001
; CURRENT APPLICATION NUMBER: US/09/798,412
; CURRENT FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/565,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)...(1720)
US-09-798-412-1
Query Match 48.7%; Score 1060.2; DB 11; Length 1879;
Best Local Similarity 76.2%; Pred. No. 1,6e-247;
Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;
QY 76 GCGGCCAAGCTCTGCTGT 135
Db 46 GTGCCCATAGCCCAAGGACACATCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 101
QY 136 CTGCTGAGGCTGATGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 195
Db 102 CTGAGAGGACATGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 161
QY 196 TCCGGGTGAGCTCACTGATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 255
Db 162 TCCGGGTGAGCTCACTGATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 221
QY 256 GCAAGTCTGAACTCTGATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 315
Db 222 GCAAGTCTGAACTCTGATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 281
QY 316 GCAAGGAGAAAGT 375
Db 282 GCAAGGAGAAAGT 341
QY 376 TGGGCTTCTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 435
Db 342 TGGGCTTCTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 401
QY 436 AGGAGCCGAGCCGAGCTTCTTCATGATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGT 495
Db 402 AGGAGCCGAGCCGAGCTTCTTCATGATGATGAGAGAGTGTGTGTGTGTGTGTGTGTGT 461
QY 496 AGCTGCTGATGATGAGT 555
Db 462 AGCTGCTGATGAGAGT 521
QY 556 TGAAGTCCAAAGATGATCTTATCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 615
Db 522 TGAAGTCCAAAGATGATCTTATCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 581
QY 616 ACCAGAGAGCTGTGAGAGGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
Db 582 ACCAGAGAGCTGTGAGAGGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 641
QY 676 GCTGCAAGAGAGAACTACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 735
Db 642 GCTGCAAGAGAGAACTACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 701
QY 736 GCGCGGCTCATGCGGAAACCTGAGCTGTGAGATTTGACCACTTAACACAGCC 795
Db 702 GAGCAGCATCATGCGGAAACCTGAGCTGTGAGATTTGAGGTGAGCAAGCTTCAAGCAGCC 761

QY 796 TCATGAGGCGAGAGCACTGCAAGTGTGAGCGCAGACAGCTGAAGCTCAGGACG 855
 DB 762 TATGAGGCGAGAGTACTGCAAGTGTGAGCGCAGACAGCTGAAGCTCAGGACG 821
 QY 856 CCATGAGAGGAGGCGCCAGACAGAGCTGTGAGAGCTGTGAGAGAGAGAGGCTGCG 915
 DB 822 CCATGAGAGGAGGCGCCAGACAGAGCTGTGAGAGCTGTGAGAGAGAGAGGCTGCG 881
 QY 916 TCAGAGGCGGAGTGTGAGAGCTGTGAGAGCTGTGAGAGAGAGAGAGAGAGAGCA 975
 DB 882 TCAGAGGCGGAGTGTGAGAGCTGTGAGAGCTGTGAGAGAGAGAGAGAGAGAGCA 941
 QY 976 GCGCCATCACTCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1035
 DB 942 GCGCCATCACTCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
 QY 1036 AGGCGCAACCACTCTCTCCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1095
 DB 1002 AGGCGCAACCACTCTCTCCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1061
 QY 1096 GGTGATGAG 1155
 DB 1062 GGTGATGAG 1121
 QY 1156 AGATGTACAAG 1215
 DB 1122 AGATGTACAAG 1181
 QY 1216 GGGACCAAG 1275
 DB 1182 GGGAC----- 1186
 QY 1276 CCGCGAGAGCTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1335
 DB 1187 ----- 1186
 QY 1336 CCCTCACTGAGAGTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1395
 DB 1187 -----CAGGCTATGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1213
 QY 1396 CAGGCAAG 1455
 DB 1214 CAGGCAAG 1273
 QY 1456 CTGGAG 1515
 DB 1274 CTGGAG 1333
 QY 1516 GCGGAG 1575
 DB 1334 GCGGAG 1393
 QY 1576 GAGATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1632
 DB 1394 GAGATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1453
 QY 1633 ACCAGAGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692
 DB 1454 ACCAGAGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1513
 QY 1693 GCTGTGAG 1752
 DB 1514 GCTGTGAG 1570
 QY 1753 CCGGCGAG 1812
 DB 1571 CCGGCGAG 1630
 QY 1813 GCGCTTCAAG 1872
 DB 1631 GCGCTTCAAG 1690
 QY 1873 GCGAG 1932

DB 1691 GCGAG 1750
 QY 1933 TGACTTGAG 1949
 DB 1751 GTAATGTGAG 1767
 RESULT 8
 US-10-325-917-1
 ; Sequence 1, Application US/10325917
 ; Publication No. US20030113787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 0734-327001
 ; CURRENT APPLICATION NUMBER: US 10/325,917
 ; PRIORITY FILING DATE: 2002-12-20
 ; PRIORITY APPLICATION NUMBER: US 09/798,412
 ; PRIORITY FILING DATE: 2001-03-02
 ; PRIORITY APPLICATION NUMBER: US 09/728,260
 ; PRIORITY FILING DATE: 2000-12-01
 ; PRIORITY APPLICATION NUMBER: US 09/685,791
 ; PRIORITY FILING DATE: 2000-10-10
 ; PRIORITY APPLICATION NUMBER: US 09/513,904
 ; PRIORITY FILING DATE: 2000-02-25
 ; PRIORITY APPLICATION NUMBER: US 09/507,533
 ; PRIORITY FILING DATE: 2000-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/168,780
 ; PRIORITY FILING DATE: 1999-12-03
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1879
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (113)...(1720)
 ; US-10-325-917-1
 Query Match 48.7%; Score 1060.2; DB 15; Length 1879;
 Best Local Similarity 76.2%; Pred. No. 1.6e-247;
 Matches 1431; Conservative 0; Mismatches 288; Indels 158; Gaps 4;
 QY 76 GCGGCGAG 135
 DB 46 GTGCGCATAGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 101
 QY 136 CTGCTGAG 195
 DB 102 CTACAG 161
 QY 196 TCAGGAG 255
 DB 162 TCAGGAG 221
 QY 256 GCAAGTCTCAAG 315
 DB 222 GCAAGTCTCAAG 281
 QY 316 GCAAG 375
 DB 282 GCAAG 341
 QY 376 TGCGCTTCTCAAG 435
 DB 342 TGCGCTTCTCAAG 401
 QY 436 AGGAG 495
 DB 402 AGGAG 461

Query Match 19.9%; Score 432; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.9e-95;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 CTGGCGAAGCAGCCAGAGCGTGTGAGAGGCTCAAGAGAGAGTCCGAGCCGAGCCG 665
DB 1 CTGGCGAAGCAGCCAGAGCGTGTGAGAGGCTCAAGAGAGAGTCCGAGCCGAGCCG 60
QY 666 GAGCTCAAGCCCTGCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 725
DB 61 GAGCTCAAGCCCTGCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 120
QY 726 GAGGAGAGAGGCGCCGCTCAAGAGAGAGTCCGAGCCGAGCCGAGCCGAGCCG 785
DB 121 GAGGAGAGAGGCGCCGCTCAAGAGAGAGTCCGAGCCGAGCCGAGCCGAGCCG 180
QY 786 AAGCAGAGCCCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 845
DB 181 AAGCAGAGCCCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 240
QY 846 CTGAGGAGAGCCCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 905
DB 241 CTGAGGAGAGCCCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 300
QY 906 AAGCCCTGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCGAGCCG 965
DB 301 AAGCCCTGCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCGAGCCG 360
QY 966 GACAGAGAGAGCCCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 1025
DB 361 GACAGAGAGAGCCCTCAAGAGAGAGAGTCAAGAGAGTCCGAGCCGAGCCGAGCCG 420
QY 1026 CACCAAGAGAGAG 1037
DB 421 CACCAAGAGAGAG 432

RESULT 12
US-10-032-159a-7
; Sequence 7, Application US/10032159A
; Publication No. US20020164703A1
; GENERAL INFORMATION:
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
; TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: P-LI 5100
; CURRENT APPLICATION NUMBER: US/10/032,159A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,457
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3744
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3744)
US-10-032-159a-7

Query Match 17.3%; Score 375.8; DB 14; Length 3744;
Best Local Similarity 56.9%; Pred. No. 2.4e-81;
Matches 817; Conservative 0; Mismatches 547; Indels 73; Gaps 4;

QY 157 ACGAAGAGATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 216
DB 26 AGGATGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 85
QY 217 TCATGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 276

DB 86 ATATCAACCTGCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 145
QY 277 ATGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 336
DB 146 ATGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 205
QY 337 TCCTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 396
DB 206 TGTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 265
QY 397 AGCTTCAATCCGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 456
DB 266 AATTATTATCCAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 325
QY 457 CCATGATCATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 516
DB 326 CCATGATCATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 385
QY 517 TGAAGTGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 555
DB 386 TGAAGTGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 445
QY 556 TGAAGTGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 615
DB 446 TGAAGTGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 505
QY 616 ACCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 675
DB 506 TCCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 565
QY 676 GCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 735
DB 566 AGGTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 625
QY 736 GCGCCGCTCATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 795
DB 626 ACATGCGGCTCATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 685
QY 796 TCATGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 855
DB 686 TGAATGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 745
QY 856 CCATGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 915
DB 746 ACATGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 805
QY 916 TCCAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 966
DB 806 TGAAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 865
QY 967 ACAAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1026
DB 866 ACTGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 925
QY 1027 ACCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1086
DB 926 GGAAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 985
QY 1087 GAGCGCTCCGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1146
DB 986 TGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1045
QY 1147 AGGAGTCAAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1206
DB 1046 AGGAGTCAAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1105
QY 1207 CCAATTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1266
DB 1106 AGCGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1127
QY 1267 GCTTGAAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1326
DB 1128 GGCTGTGCTTCCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1182

PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/507,533
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/168,780
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 3441
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-917-12

Query Match 17.1%; Score 372.2; DB 15; Length 3441;
Best Local Similarity 60.5%; Pred. No. 1.8e-80;
Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;

157 ACAGAGACGATGACGAGTCTGGAACGCTCTGGAGGGCTTCGGGTGACGCTCACTCGG 216
26 AGGATGAGAGAGAGCGCTTGTGGAGAGATGAGTGAACCGGCAATGCTCAGCGCT 85
217 TCATCGACCCCTCAGCATCAGCATCTTACCTGGGAGTGCAGAGTCTGAAACCTGATG 276
86 ATATCAACCTCTGCAAGCTCAGCCCTCAGCTGCTGATGATGATGATGATGATGATG 145
277 ATGAGAGAGAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
146 ATGAGAGTGAAGTGTCTTAAAGTCCCTTATGCTCCATTCAGATTCAGAGAGAGAG 205
337 TCCTGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
206 TGTGGACATTTCAATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 265
397 AGCTTACTTCCGAG 456
266 AATTTTATTACCAAG 325
457 CCATGATCATGAG 516
326 CCAACATTTGTGGAG 385
517 TGAAGCTGACAG 555
386 TCAAGCTGACAG 445
556 TGAAGCTTCAAG 615
446 TGGGAGAGTGTGAG 505
616 ACCAG 675
506 TCCAG 565
676 GCTGACAG 735
566 AGGTGAAG 625
735 GCGCCGCGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795
626 ACATGGGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 685
796 TCATGAG 855
686 TGAATAGATGAG 745
856 CCATGAG 915
746 ACATTTGAATTCGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 805
916 TCCAG 966
806 TGAAG 865

967 ACAG 1026
866 ACTCAG 925
1027 ACCAG 1086
926 GCGAG 985
1087 GAGGCTCCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1146
986 TCCGAG 1045
1147 AGAGCTCAAGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
1046 AGGAGTGAATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1105
1207 CCATGAG 1223
1106 AGCGGAG 1122

RESULT 15
US-09-798-412-10
Sequence 10, Application US/09798412
Publication No. US20030109428A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-327001
CURRENT APPLICATION NUMBER: US/09/798,412
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 09/728,260
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/685,791
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/513,904
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/507,533
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/168,780
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 4276
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (328) ... (3768)
US-09-798-412-10

Query Match 17.1%; Score 372.2; DB 11; Length 4276;
Best Local Similarity 60.5%; Pred. No. 1.8e-80;
Matches 664; Conservative 0; Mismatches 403; Indels 30; Gaps 2;

157 ACAGAGAGATGACGAGTGTGGAACGCTCTGGAGGGCTTCGGGTGACGCTCACTCGG 216
355 AGGATGAG 412
217 TCATGAG 276
413 ATATCAACCTCTGCAAGCTCAGCCCTCAGCTGCTGATGATGATGATGATGATG 472
277 ATGAG 336
472 ATGAG 532
337 TCCTGACATCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
533 TGTGGACATTTCAATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592

